#### SEQUENCE LISTING

#### (1) GENERAL INFORMATION:

- (i) APPLICANT: Koziel, Michael G.
  Desai, Nalini M.
  Lewis, Kelly S.
  Kramer, Vance C.
  Warren, Gregory W.
  Evola, Stephen V.
  Crossland, Lyle D.
  Wright, Martha S.
  Merlin, Ellis J.
  Launis, Karen L.
  Rothstein, Steven J.
  Bowman, Cindy G.
  Dawson, John L.
  Dunder, Erik M.
  Pace, Gary M.
  Suttie, Janet L.
- (ii) TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
- (iii) NUMBER OF SEQUENCES: 94
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Syngenta Biotechnology, Inc.
  - (B) STREET: 3054 Cornwallis Road
  - (C) CITY: Research Triangle Park
  - (D) STATE: NC
  - (E) COUNTRY: USA
  - (F) ZIP: 27709
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER:
    - (B) FILING DATE:
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 09/547,422
    - (B) FILING DATE: 11-APR-2000
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/459,504
    - (B) FILING DATE: 02-JUN-1995
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/951,715
    - (B) FILING DATE: 25-SEP-1992
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 07/772,027
    - (B) FILING DATE: 04-OCT-1991

(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Meigs, J. Timothy (B) REGISTRATION NUMBER: 38,241 (C) REFERENCE/DOCKET NUMBER: S-188051
	• • •

# (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (919)541-8587
- (B) TELEFAX: (919)541-8689

# (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3468 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Bacillus thuringiensis kurstaki
  - (B) STRAIN: HD-1
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full-length native cryIA(b)" /note= "Appears in Figures 1 and 4 as BTHKURHD."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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	TATGGGGAAT					240
	TTAACCAAAG					300
						360
	GCAATCTTTA					-
CCTACTAATC	CAGCATTAAG	AGAAGAGATG	CGTATTCAAT	TCAATGACAT	GAACAGTGCC	420
					TTTATCAGTA	480
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					TAGGCTTATT	600
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900	GGATATACTT	CACATTTGAT	ATTAGGAGTC	AGAAGGAAGT	CTCAGGGCAT	CGAGGCTCGG
960	AGGGCATCAA	ATTATTGGTC	AGAGGAGAAT	GGATGCTCAT	CCATCTATAC	AACAGTATAA
1020	ATATGGAACT	CTTTTCCGCT	CCAGAATTCA	GTTTTCGGGG	CTCCTGTAGG	ATAATGGCTT
1080	CGTGTATAGA	TAGGTCAGGG	GTTGCTCAAC	ACAACGTATT	CAGCTCCACA	ATGGGAAATG
1140	TCAACAACTA	GGATAAATAA	TTTAATATAG	TAGAAGACCT	CCACTTTATA	ACATTATCGT
1200	ATCCGCTGTA	CAAATTTGCC	GGAACCTCCT	ATTTGCTTAT	ACGGGACAGA	TCTGTTCTTG
1260	TAACAACGTG	CGCCACAGAA	GATGAAATAC	AGATTCGCTG	GCGGAACGGT	TACAGAAAAA
1320	TTCAGGCTTT	CAATGTTTCG	AGCCATGTTT	TCATCGATTA	AAGGATTTAG	CCACCTAGGC
1380	TCGTAGTGCT	CTTGGATACA	CCTATGTTCT	AATAAGAGCT	GTGTAAGTAT	AGTAATAGTA
1440	AAAATCTACT	TACCTTTAAC	ATTACACAAA	TTCATCACAA	АТАТААТТСС	GAATTTAATA
1500	AGATATTCTT	TTACAGGAGG	GGACCAGGAT	TGTCGTTAAA	CTGGAACTTC	AATCTTGGCT
1560	ACCATTATCA	ATATTACTGC	TTAAGAGTAA	GATTTCAACC	CACCTGGCCA	CGAAGAACTT
1620	CCATACATCA	ATTTĄCAATT	TCTACCACAA	TCGCTACGCT	GGGTAAGAAT	CAAAGATATC
1680	TGGGAGTAAT	CTATGAGTAG	TTTTCAGCAA	TCAGGGGAAT	GACCTATTAA	ATTGACGGAA
1740	TTCAAATGGA	CGTTTAACTT	TTTACTACTC	GACTGTAGGT	GAAGCTTTAG	TTACAGTCCG
1800	TTATATAGAT	GCAATGAAGT	TTCAATTCAG	TGCTCATGTC	TTACGTTAAG	TCAAGTGTAT
1860	AGAAAGAGCA	AATATGATTT	TTTGAGGCAG	AGAAGTAACC	TTGTTCCGGC	CGAATTGAAT
1920	AACAGATGTG	TCGGGTTAAA	TCCAATCAAA	GTTTACTTCT	TGAATGAGCT	CAAAAGGCGG
1980	TGAATTTTGT	GTTTATCTGA	TTAGTTGAGT	AGTATCCAAT	ATATTGATCA	ACGGATTATC
2040	TAGTGATGAG	CGAAGCGACT	GTCAAACATG	GTCCGAGAAA	AAAAAGAATT	CTGGATGAAA
2100	CCGTGGCTGG	GACAACTAGA	GGGATCAATA	AAACTTTAGA	TTCAAGATCC	CGGAATTTAC
2160	GAATTACGTT	TATTCAAAGA	GGCGATGACG	CATCCAAGGA	CGGATATTAC	AGAGGAAGTA
2220	AATAGATGAG	ТАТАТСАААА	CCAACGTATT	TGAGTGCTAT	GTACCTTTGA	ACGCTATTGG
2280	TAGTCAAGAC	ATATCGAAGA	TTAAGAGGGT	CCGTTACCAA	AAGCCTATAC	TCGAAATTAA
2340	GCCAGGTACG	CAGTAAATGT	AAACACGAAA	CTACAATGCC	ATTTAATTCG	TTAGAAATCT
2400	TCATTCCCAT	AATGTGCCCA	CCAATCGGAA	AGCCCCAAGT	GGCCGCTTTC	GGTTCCTTAT
2460	AGGTGTATGG	ATGAGGACTT	ACAGACTTAA	TGTTGGATGT	' TGGACATTGA	CATTTCTCCT
2520	AGAATTTCTC	TAGGAAATCT	CATGCAAGAC	GCAAGATGGC	AGATTAAGAC	GTGATATTCA
2580	GAAAAAATGG	AAAGAGCGGA	GCTCGTGTGA	AGAAGCACTA	CATTAGTAGG	GAAGAGAAAC

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TCTGTAGATG	CTTTATTTGT	AAACTCTCAA	TATGATAGAT	TACAAGCGGA	TACCAACATC	2700
GCGATGATTC	ATGCGGCAGA	TAAACGCGTT	CATAGCATTC	GAGAAGCTTA	TCTGCCTGAG	2760
CTGTCTGTGA	TTCCGGGTGT	CAATGCGGCT	ATTTTTGAAG	AATTAGAAGG	GCGTATTTTC	2820
ACTGCATTCT	CCCTATATGA	TGCGAGAAAT	GTCATTAAAA	ATGGTGATTT	TAATAATGGC	2880
TTATCCTGCT	GGAACGTGAA	AGGGCATGTA	GATGTAGAAG	AACAAAACAA	CCACCGTTCG	2940
GTCCTTGTTG	TTCCGGAATG	GGAAGCAGAA	GTGTCACAAG	AAGTTCGTGT	CTGTCCGGGT	3000
CGTGGCTATA	TCCTTCGTGT	CACAGCGTAC	AAGGAGGGAT	ATGGAGAAGG	TTGCGTAACC	3060
ATTCATGAGA	TCGAGAACAA	TACAGACGAA	CTGAAGTTTA	GCAACTGTGT	AGAAGAGGAA	3120
GTATATCCAA	ACAACACGGT	AACGTGTAAT	GATTATACTG	CGACTCAAGA	AGAATATGAG	3180
GGTACGTACA	CTTCTCGTAA	TCGAGGATAT	GACGGAGCCT	ATGAAAGCAA	TTCTTCTGTA	3240
CCAGCTGATT	-ATGCATCAGC	CTATGAAGAA	AAAGCATATA	CAGATGGACG	AAGAGACAAT	3300
CCTTGTGAAT	CTAACAGAGG	ATATGGGGAT	TACACACCAC	TACCAGCTGG	CTATGTGACA	3360
AAAGAATTAG	AGTACTTCCC	AGAAACCGAT	AAGGTATGGA	TTGAGATCGG	AGAAACGGAA	3420
GGAACATTCA	TCGTGGACAG	CGTGGAATTA	CTTCTTATGG	AGGAATAA	•	3468

#### (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3468 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full-length pure maize optimized synthetic Bt" /note= "Disclosed in Figure 3 as syn1T.mze"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

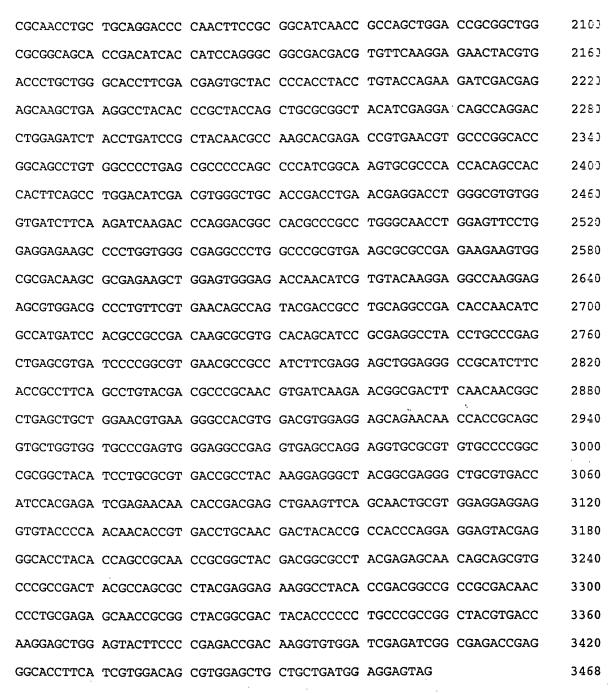
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GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG 120

AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG 180

GTGGACATCA TCTGGGGCCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC 240

GAGCAGCTGA	TCAACCAGCG	CATCGAGGAG	TTCGCCCGCA	ACCAGGCCAT	CAGCCGCCTG	300
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CCCACCAACC	CCGCCCTGCG	CGAGGAGATG	CGCATCCAGT	TCAACGACAT	GAACAGCGCC	420
CTGACCACCG	CCATCCCCCT	GTTCGCCGTG	CAGAACTACC	AGGTGCCCCT	GCTGAGCGTG	480
TACGTGCAGG	CCGCCAACCT	GCACCTGAGC	GTGCTGCGCG	ACGTGAGCGT	GTTCGGCCAG	540
CGCTGGGGCT	TCGACGCCGC	CACCATCAAC	AGCCGCTACA	ACGACCTGAC	CCGCCTGATC	600
GGCAACTACA	CCGACCACGC	CGTGCGCTGG	TACAACACCG	GCCTGGAGCG	CGTGTGGGGC	660
CCCGACAGCC	GCGACTGGAT	CCGCTACAAC	CAGTTCCGCC	GCGAGCTGAC	CCTGACCGTG	720
CTGGACATCG	TGAGCCTGTT	CCCCAACTAC	GACAGCCGCA	CCTACCCCAT	CCGCACCGTG	780
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CGCGGCAGCG	CCCAGGGCAT	CGAGGGCAGC	ATCCGCAGCC	CCCACCTGAT	GGACATCCTG	900
AACAGCATCA	CCATCTACAC	CGACGCCCAC	CGCGGCGAGT	ACTACTGGAG	CGGCCACCAG	960
ATCATGGCCA	GCCCCGTGGG	CTTCAGCGGC	CCCGAGTTCA	CCTTCCCCCT	GTACGGCACC	1020
ATGGGCAACG	CCGCCCCCA	GCAGCGCATC	GTGGCCCAGC	TGGGÇCAGGG	CGTGTACCGC	1080
ACCCTGAGCA	GCACCCTGTA	CCGCCGCCCC	TTCAACATCG	GCATCAACAA	CCAGCAGCTG	1140
AGCGTGCTGG	ACGGCACCGA	GTTCGCCTAC	GGCACCAGCA	GCAACCTGCC	CAGCGCCGTG	1200
TACCGCAAGA	GCGGCACCGT	GGACAGCCTG	GACGAGATCC	CCCCCAGAA	CAACAACGTG	1260
ccccccccc	AGGGCTTCAG	CCACCGCCTG	AGCCACGTGA	GCATGTTCCG	CAGCGGCTTC	1320
AGCAACAGCA	GCGTGAGCAT	CATCCGCGCC	CCCATGTTCA	GCTGGATCCA	CCGCAGCGCC	1380
GAGTTCAACA	ACATCATCCC	CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
AACCTGGGCA	GCGGCACCAG	CGTGGTGAAG	GGCCCCGGCT	TCACCGGCGG	CGACATCCTG	1500
CGCCGCACCA	GCCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCTGAGC	1560
CAGCGCTACC	GCGTGCGCAT	CCGCTACGCC	AGCACCACCA	ACCTGCAGTT	CCACACCAGC	1620
ATCGACGGCC	GCCCCATCAA	CCAGGGCAAC	TTCAGCGCCA	CCATGAGCAG	CGGCAGCAAC	1680
CTGCAGAGCG	GCAGCTTCCG	CACCGTGGGC	TTCACCACCC	CCTTCAACTT	CAGCAACGGC	1740
AGCAGCGTGT	TCACCCTGAG	CGCCCACGTG	TTCAACAGCG	GCAACGAGGT	GTACATCGAC	1800
CGCATCGAGT	TCGTGCCCGC	CGAGGTGACC	TTCGAGGCCG	AGTACGACCT	GGAGCGCGCC	1860
CAGAAGGCCG	TGAACGAGCT	GTTCACCAGC	AGCAACCAGA	TCGGCCTGAA	GACCGACGTG	1920
ACCGACTACC	ACATCGACCA	GGTGAGCAAC	CTGGTGGAGT	GCCTGAGCGA	CGAGTTCTGC	1980
CTGGACGAGA	AGAAGGAGCT	GAGCGAGAAG	GTGAAGCACG	CCAAGCGCCT	GAGCGACGAG	2040



#### (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1947 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO

#### (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..1947

(D) OTHER INFORMATION: /product= "Truncated synthetic

maize optimized cryIA(b) gene"

/note= "Disclosed in Figures 1, 2, 3, 4 and 5 as bssyn."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGACAACA	ACCCCAACAT	CAACGAGTGC	ATCCCCTACA	ACTGCCTGAG	CAACCCCGAG	60
GTGGAGGTGC	TGGGCGGCGA	GCGCATCGAG	ACCGGCTACA	CCCCCATCGA	CATCAGCCTG	120
AGCCTGACCC	AGTTCCTGCT	GAGCGAGTTC	GTGCCCGGCG	CCGGCTTCGT	GCTGGGCCTG	180
GTGGACATCA	TCTGGGGCAT	CTTCGGCCCC	AGCCAGTGGG	ACGCCTTCCT	GGTGCAGATC	240
GAGCAGCTGA	TCAACCAGCG	CATCGAGGAG	TTCGCCCGCA	ACCAGGCCAT	CAGCCGCCTG	300
GAGGGCCTGA	GCAACCTGTA	CCAAATCTAC	GCCGAGAGCT	TCCGCGAGTG	GGAGGCCGAC	360
CCCACCAACC	CCGCCCTGCG	CGAGGAGATG	CGCATCCAGT	TCAACGACAT	GAACAGCGCC	420
CTGACCACCG	CCATCCCCCT	GTTCGCCGTG	CAGAACTACC	AGGTGCCCCT	GCTGAGCGTG	480
TACGTGCAGG	CCGCCAACCT	GCACCTGAGC	GTGCTGCGCG	ACGTCAGCGT	GTTCGGCCAG	540
CGCTGGGGCT	TCGACGCCGC	CACCATCAAC	AGCCGCTACA	ACGACCTGAC	CCGCCTGATC	600
GGCAACTACA	CCGACCACGC	CGTGCGCTGG	TACAACACCG	GCCTGGAGCG	CGTGTGGGGT	660
CCCGACAGCC	GCGACTGGAT	CAGGTACAAC	CAGTTCCGCC	GCGAGCTGAC	CCTGACCGTG	720
CTGGACATCG	TGAGCCTGTT	CCCCAACTAC	GACAGCCGCA	CCTACCCCAT	CCGCACCGTG	780
AGCCAGCTGA	CCCGCGAGAT	TTACACCAAC	CCCGTGCTGG	AGAACTTCGA	CGGCAGCTTC	840
CGCGGCAGCG	CCCAGGGCAT	CGAGGGCAGC	ATCCGCAGCC	CCCACCTGAT	GGACATCCTG	900
AACAGCATCA	CCATCTACAC	CGACGCCCAC	CGCGGCGAGT	ACTACTGGAG	CGGCCACCAG	960
ATCATGGCCA	GCCCCGTCGG	CTTCAGCGGC	CCCGAGTTCA	CCTTCCCCCT	GTACGGCACC	1020
ATGGGCAACG	CTGCACCTCA	GCAGCGCATC	GTGGCACAGC	TGGGCCAGGG	AGTGTACCGC	1080
ACCCTGAGCA	GCACCCTGTA	CCGTCGACCT	TTCAACATCG	GCATCAACAA	CCAGCAGCTG	1140
AGCGTGCTGG	ACGGCACCGA	GTTCGCCTAC	GGCACCAGCA	GCAACCTGCC	CAGCGCCGTG	1200
TACCGCAAGA	GCGGCACCGT	GGACAGCCTG	GACGAGATCC	CCCCTCAGAA	CAACAACGTG	1260
CCACCTCGAC	AGGGCTTCAG	CCACCGTCTG	AGCCACGTGA	GCATGTTCCG	CAGTGGCTTC	1320
AGCAACAGCA	GCGTGAGCAT	CATCCGTGCA	CCTATGTTCA	GCTGGATTCA	CCGCAGTGCC	1380
GAGTTCAACA	ACATCATCCC	CAGCAGCCAA	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
AACCTGGGCA	GCGGCACCAG	CGTGGTGAAG	GGCCCCGGCT	TCACCGGCGG	CGACATCCTG	1500

CGCCGCACCA	GCCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCTGAGC	1560
CAGCGCTACC	GCGTCCGCAT	CCGCTACGCC	AGCACCACCA	ACCTGCAGTT	CCACACCAGC	1620
ATCGACGGCC	GCCCCATCAA	CCAGGGCAAC	TTCAGCGCCA	CCATGAGCAG	CGGCAGCAAC	1680
CTGCAGAGCG	GCAGCTTCCG	CACCGTGGGC	TTCACCACCC	CCTTCAACTT	CAGCAACGGC	1740
AGCAGCGTGT	TCACCCTGAG	CGCCCACGTG	TTCAACAGCG	GCAACGAGGT	GTACATCGAC	1800
CGCATCGAGT	TCGTGCCCGC	CGAGGTGACC	TTCGAGGCCG	AGTACGACCT	GGAGAGGGCT	1860
CAGAAGGCCG	TGAACGAGCT	GTTCACCAGC	AGCAACCAGA	TCGGCCTGAA	GACCGACGTG	1920
ACCGACTACC	ACATCGATCA	GGTGTAG				1947

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3468 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO

#### (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..3468
- (D) OTHER INFORMATION: /product= "Full length synthetic maize optimized" /note= "Disclosed in Figure 3 as synful.mod. This sequence is identical to flsynbt.fin as disclosed in Figure 1."

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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1	AGCCTGACCC	AGTTCCTGCT	GAGCGAGTTC	GTGCCCGGCG	CCGGCTTCGT	GCTGGGCCTG	180
(	GTGGACATCA	TCTGGGGCAT	CTTCGGCCCC	AGCCAGTGGG	ACGCCTTCCT	GGTGCAGATC	240
(	GAGCAGCTGA	TCAACCAGCG	CATCGAGGAG	TTCGCCCGCA	ACCAGGCCAT	CAGCCGCCTG	300
(	GAGGGCCTGA	GCAACCTGTA	CCAAATCTAC	GCCGAGAGCT	TCCGCGAGTG	GGAGGCCGAC	360
(	CCCACCAACC	CCGCCCTGCG	CGAGGAGATG	CGCATCCAGT	TCAACGACAT	GAACAGCGCC	420
(	CTGACCACCG	CCATCCCCCT	GTTCGCCGTG	CAGAACTACC	AGGTGCCCCT	GCTGAGCGTG	480
1	TACGTGCAGG	CCGCCAACCT	GCACCTGAGC	GTGCTGCGCG	ACGTCAGCGT	GTTCGGCCAG	540
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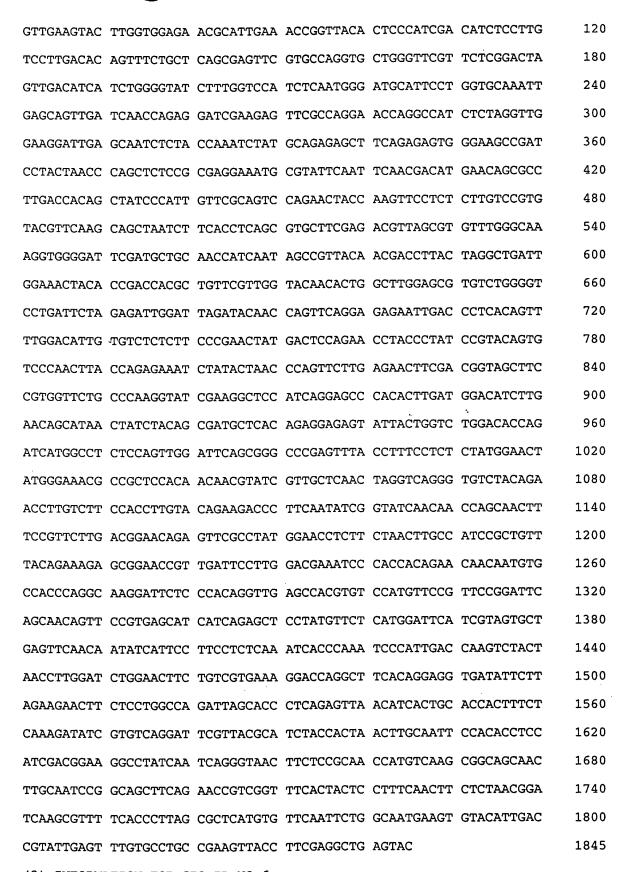
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CTGGACATCG	TGAGCCTGTT	CCCCAACTAC	GACAGCCGCA	CCTACCCCAT	CCGCACCGTG	780
AGCCAGCTGA	CCCGCGAGAT	TTACACCAAC	CCCGTGCTGG	AGAACTTCGA	CGGCAGCTTC	840
CGCGGCAGCG	CCCAGGGCAT	CGAGGGCAGC	ATCCGCAGCC	CCCACCTGAT	GGACATCCTG	900
AACAGCATCA	CCATCTACAC	CGACGCCCAC	CGCGGCGAGT	ACTACTGGAG	CGGCCACCAG	960
ATCATGGCCA	GCCCCGTCGG	CTTCAGCGGC	CCCGAGTTCA	CCTTCCCCCT	GTACGGCACC	1020
ATGGGCAACG	CTGCACCTCA	GCAGCGCATC	GTGGCACAGC	TGGGCCAGGG	AGTGTACCGC	1080
ACCCTGAGCA	GCACCCTGTA	CCGTCGACCT	TTCAACATCG	GCATCAACAA	CCAGCAGCTG	1140
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TACCGCAAGA	GCGGCACCGT	GGACAGCCTG	GACGAGATCC	CCCCTCAGAA	CAACAACGTG	1260
CCACCTCGAC	AGGGCTTCAG	CCACCGTCTG	AGCCACGTGA	GCATGTTCCG	CAGTGGCTTC	1320
AGCAACAGCA	GCGTGAGCAT	CATCCGTGCA	CCTATGTTCA	GCTGGATTCA	CCGCAGTGCC	1380
GAGTTCAACA	ACATCATCCC	CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
AACCTGGGCA	GCGGCACCAG	CGTGGTGAAG	GGCCCCGGCT	TCACCGGCGG	CGACATCCTG	1500
CGCCGCACCA	GCCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCTGAGC	1560
CAGCGCTACC	GCGTCCGCAT	CCGCTACGCC	AGCACCACCA	ACCTGCAGTT	CCACACCAGC	1620
ATCGACGGCC	GCCCCATCAA	CCAGGGCAAC	TTCAGCGCCA	CCATGAGCAG	CGGCAGCAAC	1680
CTGCAGAGCG	GCAGCTTCCG	CACCGTGGGC	TTCACCACCC	CCTTCAACTT	CAGCAACGGC	1740
AGCAGCGTGT	TCACCCTGAG	CGCCCACGTG	TTCAACAGCG	GCAACGAGGT	GTACATCGAC	1800
CGCATCGAGT	TCGTGCCCGC	CGAGGTGACC	TTCGAGGCCG	AGTACGACCT	GGAGAGGGCT	1860
CAGAAGGCCG	TGAACGAGCT	GTTCACCAGC	AGCAACCAGA	TCGGCCTGAA	GACCGACGTG	1920
ACCGACTACC	ACATCGATCA	GGTGAGCAAC	CTGGTGGAGT	GCCTGAGCGA	CGAGTTCTGC	1980
CTGGACGAGA	AGAAGGAGCT	GAGCGAGAAG	GTGAAGCACG	CCAAGCGCCT	GAGCGACGAG	2040
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CGCGGCAGCA	CCGACATCAC	CATCCAGGGC	GGCGACGACG	TGTTCAAGGA	GAACTACGTG	2160
ACCCTGCTGG	GCACCTTCGA	CGAGTGCTAC	CCCACCTACC	TGTACCAGAA	GATCGACGAG	2220
AGCAAGCTGA	AGGCCTACAC	CCGCTACCAG	CTGCGCGGCT	ACATCGAGGA	CAGCCAGGAC	2280
CTGGAGATCT	ACCTGATCCG	CTACAACGCC	AAGCACGAGA	CCGTGAACGT	GCCCGGCACC	2340
GGCAGCCTGT	GGCCCCTGAG	CGCCCCAGC	CCCATCGGCA	AGTGCGCCCA	CCACAGCCAC	2400
CACTTCAGCC	TGGACATCGA	CGTGGGCTGC	ACCGACCTGA	ACGAGGACCT	GGGCGTGTGG	2460

GTGATCTTCA	AGATCAAGAC	CCAGGACGGC	CACGCCCGCC	TGGGCAACCT	GGAGTTCCTG	2520
GAGGAGAAGC	CCCTGGTGGG	CGAGGCCCTG	GCCCGCGTGA	AGCGCGCCGA	GAAGAAGTGG	2580
CGCGACAAGC	GCGAGAAGCT	GGAGTGGGAG	ACCAACATCG	TGTACAAGGA	GGCCAAGGAG	2640
AGCGTGGACG	CCCTGTTCGT	GAACAGCCAG	TACGACCGCC	TGCAGGCCGA	CACCAACATC	2700
GCCATGATCC	ACGCCGCCGA	CAAGCGCGTG	CACAGCATTC	GCGAGGCCTA	CCTGCCCGAG	2760
CTGAGCGTGA	TCCCCGGCGT	GAACGCCGCC	ATCTTCGAGG	AGCTGGAGGG	CCGCATCTTC	2820
ACCGCCTTCA	GCCTGTACGA	CGCCCGCAAC	GTGATCAAGA	ACGGCGACTT	CAACAACGGC	2880
CTGAGCTGCT	GGAACGTGAA	GGGCCACGTG	GACGTGGAGG	AGCAGAACAA	CCACCGCAGC	2940
GTGCTGGTGG	TGCCCGAGTG	GGAGGCCGAG	GTGAGCCAGG	AGGTGCGCGT	GTGCCCCGGC	3000
CGCGGCTACA	TCCTGCGCGT	GACCGCCTAC	AAGGAGGCT	ACGGCGAGGG	CTGCGTGACC	3060
ATCCACGAGA	TCGAGAACAA	CACCGACGAG	CTCAAGTTCA	GCAACTGCGT	GGAGGAGGAG	3120
GTGTACCCCA	ACAACACCGT	GACCTGCAAC	GACTACACCG	CCACCCAGGA	GGAGTACGAG	3180
GGCACCTACA	CCAGCCGCAA	CCGCGGCTAC	GACGGCGCCT	ACGAGAGCAA	CAGCAGCGTG	3240
CCCGCCGACT	ACGCCAGCGC	CTACGAGGAG	AAGGCCTACA	CCGACGGCCG	CCGCGACAAC	3300
CCCTGCGAGA	GCAACCGCGG	CTACGGCGAC	TACACCCCCC	TGCCCGCCGG	CTACGTGACC	3360
AAGGAGCTGG	AGTACTTCCC	CGAGACCGAC	AAGGTGTGGA	TCGAGATCGG	CGAGACCGAG	3420
GGCACCTTCA	TCGTGGACAG	CGTGGAGCTG	CTGCTGATGG	AGGAGTAG		3468

#### (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1845 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..1845
- (D) OTHER INFORMATION: /note= "This is the synthetic Bt gene according to Perlak et al. as shown in Figures 4 and 5 as PMONBT."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGACAACA ACCCAAACAT CAACGAATGC ATTCCATACA ACTGCTTGAG TAACCCAGAA



(2) INFORMATION FOR SEQ ID NO:6:

	(i)	( A ( C	L) LE 3) TY C) SI	NGTH PE: RANI	i: 36 nucl	24 b Leic	STIC ase acid sing	pair 1	:s							
	(ii)								ic ac 'Synt		Lc Di	IA"				
(	(iii)	HYP	OTHE	ETICA	AL: N	10										
	otmiz	( <i>I</i> (I) (I) (ed c	O) OI	ME/F CATI HER 3"	ON: INFO	13 DRMAT	: NOI		roduc	ct= '	'Full	ler	ngth,	, mai	ize	
/r							e 6.									
		•							ID NO							
ATG Met 1	GAC Asp	CTG Leu	CTG Leu	CCC Pro 5	GAC Asp	GCC Ala	CGC Arg	ATC Ile	GAG Glu 10	GAC Asp	AGC Ser	CTG Leu	TGC Cys	ATC Ile 15	GCC Ala	48
GAG Glu	GGC Gly	AAC Asn	AAC Asn 20	ATC Ile	GAC Asp	CCC Pro	TTC Phe	GTG Val 25	AGC Ser	GCC Ala	AGC Ser	ACC Thr	GTG Val 30	CAG Gln	ACC Thr	96
									GGC Gly							144
GCC Ala	GGC Gly 50	CAG Gln	CTG Leu	GCC Ala	AGC Ser	TTC Phe 55	TAC Tyr	AGC Ser	TTC Phe	CTG Leu	GTG Val 60	GGC Gly	GAG Glu	CTG Leu	TGG Trp	192
CCC Pro 65	CGC Arg	GGC Gly	CGC Arg	GAC Asp	CAG Gln 70	TGG Trp	GAG Glu	ATC Ile	TTC Phe	CTG Leu 75	GAG Glu	CAC His	GTG Val	GAG Glu	CAG Gln 80	240
CTG Leu	ATC Ile	AAC Asn	CAG Gln	CAG Gln 85	ATC Ile	ACC Thr	GAG Glu	AAC Asn	GCC Ala 90	CGC Arg	AAC Asn	ACC Thr	GCC Ala	CTG Leu 95	GCC Ala	288
CGC Arg	CTG Leu	CAG Gln	GGC Gly 100	CTG Leu	GGC Gly	GAC Asp	AGC Ser	TTC Phe 105	CGC Arg	GCC Ala	TAC Tyr	CAG Gln	CAG Gln 110	AGC Ser	CTG Leu	336
GAG Glu	GAC Asp	TGG Trp 115	CTG Leu	GAG Glu	AAC Asn	CGC Arg	GAC Asp 120	GAC Asp	GCC Ala	CGC Arg	ACC Thr	CGC Arg 125	AGC Ser	GTG Val	CTG Leu	384
TAC Tyr	ACC Thr 130	CAG Gln	TAC Tyr	ATC Ile	GCC Ala	CTG Leu 135	GAG Glu	CTG Leu	GAC Asp	TTC Phe	CTG Leu 140	AAC Asn	GCC Ala	ATG Met	CCC Pro	432

CTG TTC GCC ATC CGC AAC CAG GAG GTG CCC CTG CTG ATG GTG TAC GCC Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala

145	150	155		160
CAG GCC GCC AAC CTG Gln Ala Ala Asn Leu 165	His Leu Leu	CTG CTG CGC Leu Leu Arg 170	GAC GCC AGC CTG Asp Ala Ser Leu 175	TTC 528 Phe
GGC AGC GAG TTC GGC Gly Ser Glu Phe Gly 180	CTG ACC AGC Leu Thr Ser	CAG GAG ATC Gln Glu Ile 185	CAG CGC TAC TAC Gln Arg Tyr Tyr 190	GAG 576 Glu
CGC CAG GTG GAG CGC Arg Gln Val Glu Arg 195	ACC CGC GAC Thr Arg Asp 200	TAC AGC GAC Tyr Ser Asp	TAC TGC GTG GAG Tyr Cys Val Glu 205	TGG 624 Trp
TAC AAC ACC GGC CTG Tyr Asn Thr Gly Leu 210				
GTG CGC TAC AAC CAG Val Arg Tyr Asn Gln 225				
CTG GTG GCC-CTG TTC Leu Val Ala Leu Phe 245	Pro Ser Tyr			
ACC AGC GCC CAG CTG Thr Ser Ala Gln Leu 260	ACC CGC GAG Thr Arg Glu	GTG TAC ACC Val Tyr Thr 265	GAC GCC ATC GGC Asp Ala Ile Gly 270	GCC 816 Ala
ACC GGC GTG AAC ATG Thr Gly Val Asn Met 275	GCC AGC ATG Ala Ser Met 280	AAC TGG TAC Asn Trp Tyr	AAC AAC AAC GCC Asn Asn Asn Ala 285	CCC 864 Pro
AGC TTC AGC GCC ATC Ser Phe Ser Ala Ile 290	GAG GCC GCC GLU Ala Ala 295	GCC ATC CGC Ala Ile Arg	AGC CCC CAC CTG Ser Pro His Leu 300	CTG 912 Leu
GAC TTC CTG GAG CAG Asp Phe Leu Glu Glr 305	CTG ACC ATC Leu Thr Ile 310	TTC AGC GCC Phe Ser Ala 315	AGC AGC CGC TGG Ser Ser Arg Trp	AGC 960 Ser 320
AAC ACC CGC CAC ATO Asn Thr Arg His Met 325	Thr Tyr Trp	CGC GGC CAC Arg Gly His 330	ACC ATC CAG AGC Thr Ile Gln Ser 335	CGC 1008 Arg
CCC ATC GGC GGC GGC Pro Ile Gly Gly Gly 340				
AGC ATC AAC CCC GTC Ser Ile Asn Pro Val 355	G ACC CTG CGC L Thr Leu Arg 360	TTC GCC AGC Phe Ala Ser	CGC GAC GTG TAC Arg Asp Val Tyr 365	CGC 1104 Arg
ACC GAG AGC TAC GCC Thr Glu Ser Tyr Ala 370				
ATC CAC GGC GTG CCC Ile His Gly Val Pro 385			Thr Asn Pro Gln	

ATC Ile	AGC Ser	GAC Asp	CGC Arg	GGC Gly 405	ACC Thr	GCC Ala	AAC Asn	TAC Tyr	AGC Ser 410	CAG Gln	CCC Pro	TAC Tyr	GAG Glu	AGC Ser 415	CCC Pro	1245
GGC Gly	CTG Leu	CAG Gln	CTG Leu 420	AAG Lys	GAC Asp	AGC Ser	GAG Glu	ACC Thr 425	GAG Glu	CTG Leu	CCC Pro	CCC Pro	GAG Glu 430	ACC Thr	ACC Thr	1295
GAG Glu	CGC Arg	CCC Pro 435	AAC Asn	TAC Tyr	GAG Glu	AGC Ser	TAC Tyr 440	AGC Ser	CAC His	CGC Arg	CTG Leu	AGC Ser 445	CAC His	ATC Ile	GGC Gly	1344
ATC Ile	ATC Ile 450	CTG Leu	CAG Gln	AGC Ser	CGC Arg	GTG Val 455	AAC Asn	GTG Val	CCC Pro	GTG Val	TAC Tyr 460	AGC Ser	TGG Trp	ACC Thr	CAC His	1392
CGC Arg 465	AGC Ser	GCC Ala	GAC Asp	CGC Arg	ACC Thr 470	AAC Asn	ACC Thr	ATC Ile	GGC Gly	CCC Pro 475	AAC Asn	CGC Arg	ATC Ile	ACC Thr	CAG Gln 480	1440
ATC Ile	CCC Pro	ATG Met	GTG Val	AAG Lys 485	GCC Ala	AGC Ser	GAG Glu	CTG Leu	CCC Pro 490	CAG Gln	GGC Gly	ACC Thr	ACC Thr	GTG Val 495	GTG Val	1483
CGC Arg	GGC Gly	CCC Pro	GGC Gly 500	TTC Phe	ACC Thr	GGC Gly	GGC Gly	GAC Asp 505	ATC Ile	CTG Leu	CGC Arg	CGC Arg	ACC Thr 510	Asn	ACC Thr	1536
GGC Gly	GGC Gly	TTC Phe 515	GGC Gly	CCC Pro	ATC Ile	CGC Arg	GTG Val 520	ACC Thr	GTG Val	AAC Asn	GGC Gly	CCC Pro 525	CTG Leu	ACC Thr	CAG Gln	1584
CGC Arg	TAC Tyr 530	CGC Arg	ATC Ile	GGC Gly	TTC Phe	CGC Arg 535	TAC Tyr	GCC Ala	AGC Ser	ACC Thr	GTG Val 540	GAC Asp	TTC Phe	GAC Asp	TTC Phe	1632
TTC Phe 545	GTG Val	AGC Ser	CGC Arg	GGC Gly	GGC Gly 550	ACC Thr	ACC Thr	GTG Val	AAC Asn	AAC Asn 555	TTC Phe	CGC Arg	TTC Phe	CTG Leu	CGC Arg 560	1680
ACC Thr	ATG Met	AAC Asn	AGC Ser	GGC Gly 565	GAC Asp	GAG Glu	CTG Leu	AAG Lys	TAC Tyr 570	GGC Gly	AAC Asn	TTC Phe	GTG Val	CGC Arg 575	CGC Arg	1728
GCC Ala	TTC Phe	ACC Thr	ACC Thr 580	Pro	TTC Phe	ACC Thr	TTC Phe	ACC Thr 585	CAG Gln	ATC Ile	CAG Gln	GAC Asp	ATC Ile 590	ATC Ile	CGC Arg	1776
ACC Thr	AGC Ser	ATC Ile 595	Gln	GGC Gly	CTG Leu	AGC Ser	GGC Gly 600	AAC Asn	GGC Gly	GAG Glu	GTG Val	TAC Tyr 605	ATC Ile	GAC Asp	AAG Lys	1824
		Ile			GTG Val											1872
GAG Glu 625	Arg	GCC Ala	CAG Gln	GAG Glu	GCC Ala 630	Val	AAC Asn	GCC Ala	CTG Leu	TTC Phe 635	ACC Thr	AAC Asn	ACC Thr	AAC Asn	CCC Pro 640	1920

CGC Arg	CGC Arg	CTG Leu	AAG Lys	ACC Thr 645	GAC Asp	GTG Val	ACC Thr	GAC Asp	TAC Tyr 650	CAC His	ATC Ile	GAC Asp	CAG Gln	GTG Val 655	AGC Ser	1965
								GAG Glu 665								2015
								GCC Ala								2064
								ACC Thr								2112
								AAC Asn						_	_	2160
								GAG Glu								2203
								GTG Val 745								2256
								CAG Gln								2304
								CGC Arg								2352
								TAC Tyr								2400
								TGG Trp								2448
								CGC Arg 825								2496
								CGC Arg								2544
								ATC Ile								2592
								GTG Val								2640
GGC	CAC	GCC	CGC	CTG	GGC	AAC	CTG	GAG	TTC	ATC	GAG	GAG	AAG	CCC	CTG	2688

Gly His Ala Arg	Leu Gly A	Asn Leu	Glu Phe 890	Ile Glu	Glu Lys	Pro 895	Leu	
CTG GGC GAG GCC Leu Gly Glu Ala 900	CTG AGC (	CGC GTG Arg Val	AAG CGC Lys Arg 905	GCC GAG Ala Glu	AAG AAG Lys Lys 910	TGG Trp	CGC Arg	2736
GAC AAG CGC GAG Asp Lys Arg Glu 915								2784
GCC AAG GAG GCC Ala Lys Glu Ala 930	Val Asp A							2832
CTG CAG GCC GAC Leu Gln Ala Asp 945								2880
GTG CAC CGC ATC Val His Arg Ile								2928
GGC GTG AAC GCC Gly Val Asn Ala 980								2976
GCC ATC AGC CTG Ala Ile Ser Leu 995			Asn Val					3024
AAC AAC GGC CTG Asn Asn Gly Leu 1010	Thr Cys	TGG AAC Trp Asn 1015	GTG AAG Val Lys	GGC CAC Gly His 1020	Val Asp	GTG Val	CAG Gln	3072
Asn Asn Gly Leu	Thr Cys 7	Trp Asn 1015 GAC CTG	Val Lys	Gly His 1020 CCC GAG	Val Asp ) TGG GAG	Val GCC	Gln GAG	3072 3120
Asn Asn Gly Leu 1010  CAG AGC CAC CAC Gln Ser His His 1025  GTG AGC CAG GCC Val Ser Gln Ala	CGC AGC CATG Ser A 1030	Trp Asn 1015 GAC CTG Asp Leu GTG TGC Val Cys	Val Lys GTG ATC Val Ile CCC GGC Pro Gly	Gly His 1020 CCC GAG Pro Glu 1035 TGC GGC Cys Gly	Val Asp ) TGG GAG Trp Glu TAC ATC Tyr Ile	Val GCC Ala CTG	GAG Glu 1040 CGC Arg	
Asn Asn Gly Leu 1010  CAG AGC CAC CAC Gln Ser His His 1025  GTG AGC CAG GCC Val Ser Gln Ala	CGC AGC (Arg Ser A 1030) GTG CGC (Val Arg Val AAG GAG (Lys Glu (Carter))	Trp Asn 1015  GAC CTG Asp Leu  GTG TGC Val Cys	Val Lys GTG ATC Val Ile CCC GGC Pro Gly 1050 GGC GAG	Gly His 1020 CCC GAG Pro Glu 1035 TGC GGC Cys Gly GGC TGC	Val Asp ) TGG GAG Trp Glu TAC ATC Tyr Ile GTG ACC	GCC Ala CTG Leu 1055	GAG Glu 1040 CGC Arg	3120
Asn Asn Gly Leu 1010  CAG AGC CAC CAC Gln Ser His His 1025  GTG AGC CAG GCC Val Ser Gln Ala  GTG ACC GCC TAC Val Thr Ala Tyr	CGC AGC (Arg Ser A 1030) GTG CGC (Val Arg Val Arg Val Arg GAG (Lys Glu (O)) AAC ACC (ARC ACC	Trp Asn 1015  GAC CTG Asp Leu  GTG TGC Val Cys  GGC TAC Gly Tyr  GAC GAG	Val Lys  GTG ATC Val Ile  CCC GGC Pro Gly 1050  GGC GAG Gly Glu 1065  CTG AAG Leu Lys	CCC GAG Pro Glu 1035 TGC GGC Cys Gly GGC TGC Gly Cys	Val Asp TGG GAG Trp Glu TAC ATC Tyr Ile GTG ACC Val Thr 1070 AAC CGC	GCC Ala  CTG Leu 1055  ATC Ile  GAG	GAG Glu 1040 CGC Arg CAC His	3120 3168
Asn Asn Gly Leu 1010  CAG AGC CAC CAC Gln Ser His His 1025  GTG AGC CAG GCC Val Ser Gln Ala  GTG ACC GCC TAC Val Thr Ala Tyr 106  GAG ATC GAG AAC Glu Ile Glu Asn	CGC AGC (Arg Ser Filoso)  GTG CGC (Val Arg Val AAC ACC (Asn Thr Filosophic CCC ACC (Pro Thr Fi	Trp Asn 1015  GAC CTG Asp Leu  GTG TGC Val Cys  GGC TAC Gly Tyr  GAC GAG Asp Glu 1080  GAC ACC	CCC GGC Pro Gly 1050 GGC GAG Gly Glu 1065 CTG AAG Leu Lys	CCC GAG Pro Glu 1035  TGC GGC Cys Gly  GGC TGC Gly Cys  TTC AAG Phe Lys	Val Asp TGG GAG Trp Glu TAC ATC Tyr Ile GTG ACC Val Thr 1070 AAC CGC Asn Arg 1085 GAC TAC Asp Tyr	GCC Ala  CTG Leu 1055  ATC Ile  GAG Glu  ACC	GAG Glu 1040 CGC Arg CAC His	3120 3168 3216
Asn Asn Gly Leu 1010  CAG AGC CAC CAC Gln Ser His His 1025  GTG AGC CAG GCC Val Ser Gln Ala  GTG ACC GCC TAC Val Thr Ala Tyr 106  GAG ATC GAG AAC Glu Ile Glu Asn 1075  GAG GAG GTG TAC Glu Glu Val Tyr	CGC AGC (Arg Ser Filoso)  GTG CGC (CVal Arg Val Arg Val Arg Val Arg Val Arg Val Color (CVal Arg Val Arg Val Arg Val Arg Val AAC ACC (Arg Glu Color (CVal Arg Val Arg V	Trp Asn 1015  GAC CTG Asp Leu  GTG TGC Val Cys  GGC TAC Gly Tyr  GAC GAG Asp Glu 1080  GAC ACC Asp Thr 1095	CCC GGC Pro Gly 1050 GGC GAG Gly Glu 1065 CTG AAG Leu Lys GGC ACC Gly Thr	CCC GAG Pro Glu 1035  TGC GGC Cys Gly  GGC TGC Gly Cys  TTC AAG Phe Lys  TGC AAC Cys Asn 1100 TGC AAC	Val Asp TGG GAG Trp Glu TAC ATC Tyr Ile GTG ACC Val Thr 1070 AAC CGC Asn Arg 1085 GAC TAC Asp Tyr AGC CGC	GCC Ala  CTG Leu 1055  ATC Ile  GAG Glu  ACC Thr  AAC Asn	GAG Glu 1040 CGC Arg CAC His GAG Glu GCC Ala	3120 3168 3216 3264

				112	5				113	0				113	5	
			TAC Tyr 114	Glu					Thr					Asp		3456
			Tyr					Val					Val		GCC Ala	3504
		Val	ACC Thr				Glu					Thr				3552
	Ile		ATC Ile			Thr					Ile					3600
			CTG Leu		Glu		TAG									3624
(2)	INF	ORMA?	FION	FOR	SEQ	ID 1	NO:7:	•								
		(i) S	(B)	LEN TYI	NGTH: PE: a	: 120 amino		nino id		is				4		
	( :	ii) M	40LEC	CULE	TYPE	E: pi	rotei	in								
			OLEC SEQUE						) ID	NO: 7	7:					
Met 1	(2	ci) S		ENCE	DESC	CRIPT	rion:	: SE(				Leu	Cys	Ile 15	Ala	
1	() Asp	ci) S Leu	SEQUE	Pro 5	DESC Asp	CRIPT Ala	TION: Arg	: SE(	Glu 10	Asp	Ser			15		
1 Glu	Asp Gly	ci) { Leu Asn	SEQUE Leu Asn	Pro 5	DESC Asp Asp	CRIPT Ala Pro	PION:	: SE( Ile Val 25	Glu 10 Ser	Asp Ala	Ser Ser	Thr	Val 30	15 Gln	Thr	
1 Glu Gly	Asp Gly Ile	Leu Asn Asn 35	EEQUE Leu Asn 20	Pro 5 Ile Ala	DESC Asp Asp Gly	Ala Pro Arg	Phe Ile 40	: SE( Ile Val 25 Leu	Glu 10 Ser	Asp Ala Val	Ser Ser Leu	Thr Gly 45	Val 30 Val	15 Gln Pro	Thr Phe	
Glu Gly Ala	Asp Gly Ile Gly 50	Leu Asn Asn 35	Leu Asn 20	Pro 5 Ile Ala Ala	DESC Asp Asp Gly Ser	Ala Pro Arg Phe 55	Phe Ile 40	: SEQ Ile Val 25 Leu Ser	Glu 10 Ser Gly Phe	Asp Ala Val Leu	Ser  Ser  Leu  Val 60	Thr Gly 45 Gly	Val 30 Val Glu	15 Gln Pro Leu	Thr Phe Trp	
Glu Gly Ala Pro 65	Asp Gly Ile Gly 50	Leu Asn Asn Scln Gly	Leu Asn 20 Ile	Pro 5 Ile Ala Ala Asp	Asp Asp Gly Ser Gln 70	Ala Pro Arg Phe 55	Phe Ile 40 Tyr	: SEQ Ile Val 25 Leu Ser	Glu 10 Ser Gly Phe	Asp Ala Val Leu 75	Ser Leu Val 60 Glu	Thr Gly 45 Gly His	Val 30 Val Glu Val	15 Gln Pro Leu Glu	Thr Phe Trp Gln 80	
Glu Gly Ala Pro 65 Leu	Asp Gly Ile Gly 50 Arg	Leu Asn Asn 35 Gln Gly Asn	Leu Asn 20 Ile Leu Arg	Pro 5 Ile Ala Ala Asp Gln 85	Asp Asp Gly Ser Gln 70 Ile	Ala Pro Arg Phe 55 Trp	Phe Ile 40 Tyr Glu	: SEC Ile Val 25 Leu Ser Ile Asn	Glu 10 Ser Gly Phe Phe	Asp Ala Val Leu 75 Arg	Ser Leu Val 60 Glu Asn	Thr Gly 45 Gly His	Val 30 Val Glu Val	15 Gln Pro Leu Glu Leu 95	Thr Phe Trp Gln 80 Ala	
Glu Gly Ala Pro 65 Leu Arg	Asp Gly Ile Gly 50 Arg Ile	Leu Asn Asn 35 Gln Gly Asn Gln	Leu Asn 20 Ile Leu Arg Gln	Pro 5 Ile Ala Ala Asp Gln 85 Leu	Asp Asp Gly Ser Gln 70 Ile	Pro Arg Phe 55 Trp Thr	Phe Ile 40 Tyr Glu Glu Ser	Val 25 Leu Ser Ile Asn	Glu 10 Ser Gly Phe Phe Ala 90 Arg	Asp Ala Val Leu 75 Arg	Ser  Ser  Leu  Val 60  Glu  Asn	Thr Gly 45 Gly His Thr	Val 30 Val Glu Val Ala Gln 110	15 Gln Pro Leu Glu Leu 95 Ser	Thr Phe Trp Gln 80 Ala	

Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala 155 Gln Ala Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Leu Phe 165 170 Gly Ser Glu Phe Gly Leu Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu 185 Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp Tyr Cys Val Glu Trp Tyr Asn Thr Gly Leu Asn Ser Leu Arg Gly Thr Asn Ala Ala Ser Trp 215 Val Arg Tyr Asn Gln Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Ala Thr Gly Val Asn Met Ala Ser Met Asn Trp Tyr Asn Asn Asn Ala Pro Ser Phe Ser Ala Ile Glu Ala Ala Ala Ile Arg Ser Pro His Leu Leu Asp Phe Leu Glu Gln Leu Thr Ile Phe Ser Ala Ser Ser Arg Trp Ser Asn Thr Arg His Met Thr Tyr Trp Arg Gly His Thr Ile Gln Ser Arg Pro Ile Gly Gly Leu Asn Thr Ser Thr His Gly Ala Thr Asn Thr Ser Ile Asn Pro Val Thr Leu Arg Phe Ala Ser Arg Asp Val Tyr Arg 355 Thr Glu Ser Tyr Ala Gly Val Leu Leu Trp Gly Ile Tyr Leu Glu Pro Ile His Gly Val Pro Thr Val Arg Phe Asn Phe Thr Asn Pro Gln Asn 385 395 Ile Ser Asp Arg Gly Thr Ala Asn Tyr Ser Gln Pro Tyr Glu Ser Pro Gly Leu Gln Leu Lys Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Ile Ile Leu Gln Ser Arg Val Asn Val Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln

465	470		475	480
Ile Pro Met Val 1	Lys Ala Ser 485	Glu Leu Pro 490	Gln Gly Thr	Thr Val Val 495
Arg Gly Pro Gly 1	Phe Thr Gly	Gly Asp Ile 505	Leu Arg Arg	Thr Asn Thr 510
Gly Gly Phe Gly 1 515	Pro Ile Arg	Val Thr Val 520	Asn Gly Pro 525	Leu Thr Gln
Arg Tyr Arg Ile (	Gly Phe Arg 535	Tyr Ala Ser	Thr Val Asp 540	Phe Asp Phe
Phe Val Ser Arg ( 545	Gly Gly Thr 550	Thr Val Asn	Asn Phe Arg 555	Phe Leu Arg 560
Thr Met Asn Ser (	Gly Asp Glu 565	Leu Lys Tyr 570	Gly Asn Phe	Val Arg Arg 575
Ala Phe Thr Thr 1	Pro Phe Thr	Phe Thr Gln 585	Ile Gln Asp	Ile Ile Arg 590
Thr Ser Ile Gln (	Gly Leu Ser	Gly Asn Gly 600	Glu Val Tyr 605	Ile Asp Lys
Ile Glu Ile Ile 1 610	Pro Val Thr 615	Ala Thr Phe	Glu Ala Glu 620 .	Tyr Asp Leu
Glu Arg Ala Gln (	Glu Ala Val 630	Asn Ala Leu	Phe Thr Asn 635	Thr Asn Pro 640
Arg Arg Leu Lys	Thr Asp Val 645	Thr Asp Tyr 650	His Ile Asp	Gln Val Ser 655
Asn Leu Val Ala (	Cys Leu Ser	Asp Glu Phe 665	Cys Leu Asp	Glu Lys Arg 670
Glu Leu Leu Glu 1 675	Lys Val Lys	Tyr Ala Lys 680	Arg Leu Ser 685	Asp Glu Arg
Asn Leu Leu Gln 7	Asp Pro Asn 695	Phe Thr Ser	Ile Asn Lys 700	Gln Pro Asp
Phe Ile Ser Thr 7	Asn Glu Gln 710	Ser Asn Phe	Thr Ser Ile 715	His Glu Gln 720
Ser Glu His Gly	Trp Trp Gly 725	Ser Glu Asn 730	Ile Thr Ile	Gln Glu Gly 735
Asn Asp Val Phe 1740	Lys Glu Asn	Tyr Val Thr 745	Leu Pro Gly	Thr Phe Asn 750
Glu Cys Tyr Pro 5	Thr Tyr Leu	Tyr Gln Lys 760	Ile Gly Glu 765	Ser Glu Leu
Lys Ala Tyr Thr 7	Arg Tyr Gln 775	Leu Arg Gly	Tyr Ile Glu 780	Asp Ser Gln
Asp Leu Glu Ile 7	Tyr Leu Ile 790	Arg Tyr Asn	Ala Lys His 795	Glu Thr Leu 800

Asp Val Pro Gly Thr Glu Ser Leu Trp Pro Leu Ser Val Glu Ser Pro 805 810 815

Ile Gly Arg Cys Gly Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp 820 825 830

Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His 835 840 845

His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu 850 855 860

His Glu Asn Leu Gly Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu 865 870 875 880

Gly His Ala Arg Leu Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu 885 890 895

Leu Gly Glu Ala Leu Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg 900 905 910

Asp Lys Arg-Glu Lys Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu 915 920 925

Ala Lys Glu Ala Val Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Arg 930 935 940

Leu Gln Ala Asp Thr Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu 945 950 955 960

Val His Arg Ile Arg Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro 965 970 975

Gly Val Asn Ala Glu Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr 980 985 990

Ala Ile Ser Leu Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe 995 1000 1005

Asn Asn Gly Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln 1010 1015 1020

Gln Ser His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu 1025 1030 1035 1040

Val Ser Gln Ala Val Arg Val Cys Pro Gly Cys Gly Tyr Ile Leu Arg 1045 1050 1055

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His 1060 1065 1070

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Arg Glu Glu 1075 1080 1085

Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr Ala 1090 1095 1100

His Gln Gly Thr Ala Gly Cys Ala Asp Ala Cys Asn Ser Arg Asn Ala 1105 1110 1115 1120

Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val As 1125 1130 11	n Tyr 35
Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg As 1140 1145 1150	p Asn
His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pr 1155 1160 1165	o Ala
Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Th 1170 1175 1180	r Val
Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Se 1185 1190 1195	r Val 1200
Glu Leu Leu Met Glu Glu 1205	
(2) INFORMATION FOR SEQ ID NO:8:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 3468 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "Synthetic DNA" .	
(iii) HYPOTHETICAL: NO	
<pre>(ix) FEATURE:</pre>	ybrid,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys 1210 1215 1220	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Th 1225 1230 1235	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu 1240 1245 1250	G AGC 144 1 Ser 1255
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG G	

1285

240

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1260 1265 1270

TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile

1280

1275

GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1290 1295 1300	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG  Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  1305 1310 1315	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1320 1325 1330 1335	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1340 1345 1350	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG  Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  1355 1360 1365	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln-Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1370 1375 1380	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1385 1390 1395	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1400 1405 1410 1415	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1420 1425 1430	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1435	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1450 1455 1460	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG  Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  1465 1470 1475	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1480 1485 1490 1495	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1500 1505 1510	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1515 1520 1525	960

ATC /	ATG Met	GCC Ala 1530	Ser	CCC Pro	GTC Val	GGC Gly	TTC Phe 1535	Ser	GGC Gly	CCC Pro	GAG Glu	TTC Phe 1540	Thr	TTC Phe	CCC Pro	1008
CTG ' Leu '	TAC Tyr 1545	Gly	ACC Thr	ATG Met	GGC Gly	AAC Asn 1550	Ala	GCA Ala	CCT Pro	CAG Gln	CAG Gln 1555	Arg	ATC Ile	GTG Val	GCA Ala	1056
CAG Gln 1560	Leu	GGC Gly	CAG Gln	GGA Gly	GTG Val 1565	Tyr	CGC Arg	ACC Thr	CTG Leu	AGC Ser 1570	Ser	ACC Thr	CTG Leu	TAC Tyr	CGT Arg 1575	1104
CGA Arg	CCT Pro	TTC Phe	AAC Asn	ATC Ile 1580	Gly	ATC Ile	AAC Asn	AAC Asn	CAG Gln 1585	Gln	CTG Leu	AGC Ser	GTG Val	CTG Leu 1590	Asp	1152
GGC Gly	ACC Thr	GAG Glu	TTC Phe 1595	Ala	TAC Tyr	GGC Gly	ACC Thr	AGC Ser 1600	Ser	AAC Asn	CTG Leu	CCC Pro	AGC Ser 1605	Ala	GTG Val	1200
TAC Tyr	CGC Arg	AAG Lys 1610	Ser	GGC Gly	ACC Thr	GTG Val	GAC Asp 1615	Ser	CTG Leu	GAC Asp	GAG Glu	ATC Ile 1620	Pro	CCT Pro	CAG Gln	1248
	AAC Asn 1625	Asn	GTG Val	CCA Pro	CCT Pro	CGA Arg 1630	Gln	GGC Gly	TTC Phe	AGC Ser	CAC His 1635	Arg	CTG Leu	AGC Ser	CAC His	1296
GTG Val 1640	Ser	ATG Met	TTC Phe	CGC Arg	AGT Ser 1645	Gly	TTC Phe	AGC Ser	AAC Asn	AGC Ser 1650	Ser	GTG Val	AGC Ser	ATC Ile	ATC Ile 1655	1344
CGT Arg	GCA Ala	CCT Pro	ATG Met	TTC Phe 1660	AGC Ser O	TGG Trp	ATT Ile	CAC His	CGC Arg 1665	Ser	GCC Ala	GAG Glu	TTC Phe	AAC Asn 1670	Asn	1392
ATC Ile	ATC Ile	CCC Pro	AGC Ser 1675	Ser	CAG Gln	ATC Ile	ACC Thr	CAG Gln 1680	Ile	CCC Pro	CTG Leu	ACC Thr	AAG Lys 1689	Ser	ACC Thr	1440
AAC Asn	CTG Leu	GGC Gly 1690	Ser	GGC Gly	ACC Thr	AGC Ser	GTG Val 169	Val	AAG Lys	GGC Gly	CCC Pro	GGC Gly 1700	Phe	ACC Thr	GGC Gly	1488
Gly	GAC Asp 1705	Ile	CTG Leu	CGC Arg	CGC Arg	ACC Thr 171	Ser	CCC Pro	GGC Gly	CAG Gln	ATC Ile 1715	Ser	ACC Thr	CTG Leu	CGC Arg	1536
GTG Val 1720	Asn	ATC Ile	ACC Thr	GCC Ala	CCC Pro 172	Leu	AGC Ser	CAG Gln	CGC Arg	TAC Tyr 173	Arg	GTC Val	CGC Arg	ATC Ile	CGC Arg 1735	1584
TAC Tyr	GCC Ala	AGC Ser	ACC Thr	ACC Thr 174	AAC Asn 0	CTG Leu	CAG Gln	TTC Phe	CAC His 174	Thr	AGC Ser	ATC Ile	GAC Asp	GGC Gly 1750	Arg	1632
CCC Pro	ATC Ile	AAC Asn	CAG Gln 175	Gly	AAC Asn	TTC Phe	AGC Ser	GCC Ala 176	Thr	ATG Met	AGC Ser	AGC Ser	GGC Gly 176	Ser	AAC Asn	1680
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC	1728

	er Gly S 770	er Phe Arq	Thr Val	Gly Phe	Thr Thr I 1780	Pro Phe	Asn
TTC AGC A Phe Ser A 1785	sn Gly S	GC AGC GTO er Ser Val 179	. Phe Thr	CTG AGC Leu Ser	GCC CAC ( Ala His \ 1795	GTG TTC /al Phe	AAC 1776 Asn
AGC GGC A Ser Gly A 1800	AC GAG G sn Glu V	TG TAC ATO al Tyr Ile 1805	GAC CGC Asp Arg	ATC GAG Ile Glu 181	TTC GTG ( Phe Val I	CCC GCC Pro Ala	GAG 1824 Glu 1815
GTG ACC T Val Thr P	he Glu A	CC GAG TAG la Glu Ty: 820	GAC CTG Asp Leu	GAG AGG Glu Arg 1825	GCT CAG A	AAG GCC Lys Ala 1830	Val
AAC GAG C Asn Glu L	TG TTC A eu Phe T 1835	CC AGC AGC hr Ser Se	C AAC CAG Asn Gln 184	Ile Gly	CTG AAG A	ACC GAC Thr Asp 1845	GTG 1920 Val
Thr Asp T	AC CAC A Yr His I	TC GAT CA	A GTA TCC n Val Ser 1855	AAT TTA Asn Leu	GTT GAG 1 Val Glu ( 1860	TGT TTA Cys Leu	TCT 1968 Ser
GAT GAA T Asp Glu P 1865	TTT TGT C	TG GAT GA eu Asp Gl	ı Lys Lys	GAA TTG Glu Leu	G TCC GAG A Ser Glu I 1875	AAA GTC Lys Val	AAA 2016 Lys
CAT GCG A His Ala L 1880	AAG CGA C Ys Arg L	TT AGT GA eu Ser As 1885	r GAG CGG o Glu Arg	AAT TTA Asn Leu 189	CTT CAA ( Leu Gln 2	GAT CCA Asp Pro	AAC 2064 Asn 1895
TTT AGA G	Sly Ile A	AT AGA CA Asn Arg Gl .900	A CTA GAC n Leu Asp	CGT GGC Arg Gly 1905	TGG AGA (	GGA AGT Gly Ser 1910	Thr
GAT ATT A Asp Ile T	ACC ATC C Thr Ile G 1915	CAA GGA GG Gln Gly Gl	C GAT GAC y Asp Asp 192	Val Phe	AAA GAG	AAT TAC Asn Tyr 1925	GTT 2160 Val
Thr Leu I	Leu Gly T	hr Phe As	o Glu Cys	Tyr Pro	A ACG TAT of Thr Tyr 1940	Leu Tyr	Gln
AAA ATA G Lys Ile A 1945	GAT GAG 1 Asp Glu S	CCG AAA TT Ser Lys Le 19	u Lys Ala	TAT ACC	C CGT TAC Arg Tyr 1955	CAA TTA Gln Leu	AGA 2256 Arg
GGG TAT A Gly Tyr I 1960	ATC GAA ( Ile Glu <i>I</i>	GAT AGT CA Asp Ser Gl 1965	A GAC TTA n Asp Lei	A GAA ATO 1 Glu Ile 197	TAT TTA . Tyr Leu 70	ATT CGC Ile Arg	TAC 2304 Tyr 1975
AAT GCC A Asn Ala I	Lys His (	GAA ACA GT Glu Thr Va 1980	A AAT GTO 1 Asn Val	G CCA GGT L Pro Gly 1985	ACG GGT Thr Gly	TCC TTA Ser Leu 1990	Trp
CCG CTT ? Pro Leu ?	TCA GCC ( Ser Ala 1 1995	CCA AGT CC Pro Ser Pr	A ATC GGA o Ile Gly 200	y Lys Cys	T GCC CAT S Ala His	CAT TCC His Ser 2005	CAT 2400 His
CAT TTC THIS Phe	TCC TTG ( Ser Leu <i>l</i>	GAC ATT GA Asp Ile As	T GTT GGA p Val Gly	A TGT ACA V Cys Thi	A GAC TTA r Asp Leu	AAT GAG Asn Glu	GAC 2448 Asp

2010 2015 2020

TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC CAT GCA Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala 2025 2030 2035	2496
AGA CTA GGA AAT CTA GAA TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu 2040 2045 2050 2055	2544
GCA CTA GCT CGT GTG AAA AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg 2060 2065 2070	2592
GAA AAA TTG GAA TGG GAA ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu 2075 2080 2085	2640
TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala 2090 2095 2100	2688
GAT ACC AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser 2105 2110 2115	2736
ATT CGA GAA GCT TAT CTG CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn 2120 2135	2784
GCG GCT ATT TTT GAA GAA TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser 2140 2145 2150	2832
CTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly 2155 2160 2165	2880
TTA TCC TGC TGG AAC GTG AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn 2170 2175 2180	2928
AAC CAC CGT TCG GTC CTT GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser 2185 2190 2195	2976
CAA GAA GTT CGT GTC TGT CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr 2200 2205 2210 2215	3024
GCG TAC AAG GAG GGA TAT GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile 2220 2225 2230	3072
GAG AAC AAT ACA GAC GAA CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu 2235 2240 2245	3120
GTA TAT CCA AAC AAC ACG GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln 2250 2255 2260	3168

GAA GAA TAT GAG GGT Glu Glu Tyr Glu Gly 2265	ACG TAC ACT TCT CG Thr Tyr Thr Ser Are 2270	r AAT CGA GGA TAT G g Asn Arg Gly Tyr A 2275	AC GGA 3216 sp Gly
GCC TAT GAA AGC AAT Ala Tyr Glu Ser Asn 2280	TCT TCT GTA CCA GC Ser Ser Val Pro Al 2285	r GAT TAT GCA TCA G a Asp Tyr Ala Ser A 2290	CC TAT 3264 la Tyr 2295
GAA GAA AAA GCA TAT Glu Glu Lys Ala Tyr 2300	Thr Asp Gly Arg Ar	g Asp Asn Pro Cys G	AA TCT 3312 lu Ser 310
AAC AGA GGA TAT GGG Asn Arg Gly Tyr Gly 2315	GAT TAC ACA CCA CT Asp Tyr Thr Pro Le 2320	A CCA GCT GGC TAT G u Pro Ala Gly Tyr V 2325	TG ACA 3360 al Thr
AAA GAA TTA GAG TAC Lys Glu Leu Glu Tyr 2330	TTC CCA GAA ACC GA Phe Pro Glu Thr As 2335	T AAG GTA TGG ATT G p Lys Val Trp Ile G 2340	AG ATC 3408 lu Ile
GGA GAA ACG GAA GGA Gly Glu Thr Glu Gly 2345	ACA TTC ATC GTG GA Thr Phe Ile Val As 2350	C AGC GTG GAA TTA C p Ser Val Glu Leu L 2355	TT CTT 3456 eu Leu
ATG GAG GAA TAA Met Glu Glu 2360		, ,	3468

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1155 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
- Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
- Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
- Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
- Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
- Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80
- Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
- Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 135 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 265 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 425 420

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 475 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 535 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 555 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 585 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 695 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr

		755					760					765			
Asn	Ala 770	Lys	His	Glu	Thr	Val 775	Asn	Val	Pro	Gly	Thr 780	Gly	Ser	Leu	Trp
Pro 785	Leu	Ser	Ala	Pro	Ser 790	Pro	Ile	Gly	Lys	Cys 795	Ala	His	His	Ser	His 800
His	Phe	Ser	Leu	Asp 805	Ile	Asp	Val	Gly	Cys 810	Thr	Asp	Leu	Asn	Glu 815	Asp
Leu	Gly	Val	Trp 820	Val	Ile	Phe	Lys	Ile 825	Lys	Thr	Gln	Asp	Gly 830	His	Ala
Arg	Leu	Gly 835	Asn	Leu	Glu	Phe	Leu 840	Glu	Glu	Lys	Pro	Leu 845	Val	Gly	Glu
Ala	Leu 850	Ala	Arg	Val	Lys	Arg 855	Ala	Glu	Lys	Lys	Trp 860	Arg	Asp	Lys	Arg
Glu 865	Lys	Leu	Glu	Trp	Glu 870	Thr	Asn	Ile	Val	Tyr 875	Lys	Glu	Ala	Lys	Glu 880
Ser	Val	Asp	Ala	Leu 885	Phe	Val	Asn	Ser	Gln 890	Tyr	Asp	Arg	Leu	Gln 895	Ala
Asp	Thr	Asn	Ile 900	Ala	Met	Ile	His	Ala 905	Ala	Asp	Lys	Arg 	Val 910		Ser
Ile	Arg	Glu 915	Ala	Tyr	Leu	Pro	Glu 920	Leu	Ser	Val	Ile	Pro 925	Gly	Val	Asn
Ala	Ala 930	Ile	Phe	Glu	Glu	Leu 935	Glu	Gly	Arg	Ile	Phe 940	Thr	Ala	Phe	Ser
Leu 945	Tyr	Asp	Ala	Arg	Asn 950	Val	Ile	Lys	Asn	Gly 955	Asp	Phe	Asn	Asn	Gly 960
Leu	Ser	Cys	Trp	Asn 965	Val	Lys	Gly	His	Val 970	Asp	Val	Glu	Glu	Gln 975	Asn
Asn	His	Arg	Ser 980	Val	Leu	Val	Val	Pro 985	Glu	Trp	Glu	Ala	Glu 990	Val	Ser
Gln	Glu	Val 995	Arg	Val	Cys	Pro	Gly 1000		Gly	Tyr	Ile	Leu 1005		Val	Thr
Ala	Tyr 1010		Glu	Gly	Tyr	Gly 1015		Gly	Cys	Val	Thr 1020		His	Glu	Ile
Glu 1025		Asn	Thr	Asp	Glu 1030	Leu )	Lys	Phe	Ser	Asn 1035		Val	Glu	Glu	Glu 1040
Val	Tyr	Pro	Asn	Asn 1045		Val	Thr	Cys	Asn 1050		Tyr	Thr	Ala	Thr 1055	
Glu	Glu	Tyr	Glu 1060		Thr	Tyr	Thr	Ser 1065		Asn	Arg	Gly	Tyr 1070		Gly
Ala	Tyr	Glu		Asn	Ser	Ser	Val		Ala	Asp	Tyr	Ala		Ala	Tyr

Glu Glu Lys 1090	Ala Tyr Thr	Asp Gly Arg 1095	Arg Asp Asn 1100		Ser							
Asn Arg Gly	Tyr Gly Asp		Leu Pro Ala 1115	Gly Tyr Val	Thr 1120							
Lys Glu Leu	Glu Tyr Phe 1125	Pro Glu Thr	Asp Lys Val	Trp Ile Glu 113	. Ile 5							
Gly Glu Thr	Glu Gly Thr 1140	Phe Ile Val	Asp Ser Val	Glu Leu Leu 1150	Leu							
Met Glu Glu 1155												
(2) INFORMAT	(2) INFORMATION FOR SEQ ID NO:10:											
( <i>I</i> (E	QUENCE CHARAGE A) LENGTH: 3! B) TYPE: nuc C) STRANDEDN: D) TOPOLOGY:	546 base pair leic acid ESS: single	rs									
	LECULE TYPE: A) DESCRIPTION		ic acid "Synthetic Di	NA"								
(iii) HY	POTHETICAL:	NO										
(1 (1 maize opt:	A) NAME/KEY: B) LOCATION: D) OTHER INF imized heat	13543 ORMATION: /p: stable cryIA	roduct= "Ful? (b)" contained in		brid,							
(xi) SE	QUENCE DESCR	IPTION: SEQ	ID NO:10:									
			TGC ATC CCC Cys Ile Pro 1165		Leu							
			GGC GAG CGC Gly Glu Arg 0									
	Ile Asp Ile		CTG ACC CAG Leu Thr Gln									
			CTG GGC CTG Leu Gly Leu 121	Val Asp Ile								
		Ser Gln Trp	GAC GCC TTC Asp Ala Phe 1230									
GAG CAG CTG	ATC AAC CAG	CGC ATC GAG	GAG TTC GCC	CGC AAC CAC	GCC 288							

Glu Gln Leu	Ile Asn Gln 1240	Arg Ile	Glu Glu 1245		Arg Asn	Gln Ala 1250	
ATC AGC CGC Ile Ser Arg						Ala Glu	336
AGC TTC CGC Ser Phe Arg 1270	Glu Trp Glu		Pro Thr				384
GAG ATG CGC Glu Met Arg 1285					Leu Thr		432
ATC CCC CTG Ile Pro Leu 1300		Gln Asn					480
TAC GTG CAG Tyr Val Gln				Val Leu			528
GTG TTC GGC Val Phe Gly						Ser Arg	576
TAC AAC GAC Tyr Asn Asp 1350	Leu Thr Arg		Gly Asn				624
CGC TGG TAC Arg Trp Tyr 1365		Leu Glu			Pro Asp		672
		1370		13/3	•		
GAC TGG ATC Asp Trp Ile 1380		CAG TTC Gln Phe		GAG CTG	ACC CTG		720
GAC TGG ATC Asp Trp Ile 1380 CTG GAC ATC Leu Asp Ile	Arg Tyr Asn 138 GTG AGC CTG	CAG TTC Gln Phe 5 TTC CCC Phe Pro	Arg Arg  AAC TAC Asn Tyr	GAG CTG Glu Leu 1390 GAC AGC Asp Ser	ACC CTG Thr Leu CGC ACC Arg Thr	Thr Val 1395 TAC CCC Tyr Pro	720 768
GAC TGG ATC Asp Trp Ile 1380 CTG GAC ATC Leu Asp Ile	Arg Tyr Asn 138 GTG AGC CTG Val Ser Leu 1400 GTG AGC CAG	CAG TTC Gln Phe 5  TTC CCC Phe Pro	AAC TAC Asn Tyr 1405	GAG CTG Glu Leu 1390  GAC AGC Asp Ser ATT TAC	ACC CTG Thr Leu  CGC ACC Arg Thr  ACC AAC	Thr Val 1395 TAC CCC Tyr Pro 1410 CCC GTG Pro Val	
GAC TGG ATC Asp Trp Ile 1380  CTG GAC ATC Leu Asp Ile  ATC CGC ACC	Arg Tyr Asn 138  GTG AGC CTG Val Ser Leu 1400  GTG AGC CAG Val Ser Gln 1415  TTC GAC GGC Phe Asp Gly	CAG TTC Gln Phe 5  TTC CCC Phe Pro  CTG ACC Leu Thr	ARG ARG  AAC TAC ASN Tyr 1405  CGC GAG ARG Glu 1420  CGC GGC ARG Gly	GAG CTG Glu Leu 1390  GAC AGC Asp Ser  ATT TAC Ile Tyr  AGC GCC	ACC CTG Thr Leu  CGC ACC Arg Thr  ACC AAC Thr Asn 1425 CAG GGC	Thr Val 1395  TAC CCC Tyr Pro 1410  CCC GTG Pro Val  ATC GAG	768
GAC TGG ATC Asp Trp Ile 1380  CTG GAC ATC Leu Asp Ile  ATC CGC ACC Ile Arg Thr  CTG GAG AAC Leu Glu Asn	Arg Tyr Asn 138 GTG AGC CTG Val Ser Leu 1400 GTG AGC CAG Val Ser Gln 1415 TTC GAC GGC Phe Asp Gly	CAG TTC Gln Phe 5  TTC CCC Phe Pro  CTG ACC Leu Thr  AGC TTC Ser Phe 1435 CAC CTG	ARG ARG  AAC TAC ASN Tyr 1405  CGC GAG ARG Glu 1420  CGC GGC ARG Gly  ATG GAC	GAG CTG Glu Leu 1390  GAC AGC Asp Ser  ATT TAC Ile Tyr  AGC GCC Ser Ala  ATC CTG	ACC CTG Thr Leu  CGC ACC Arg Thr  ACC AAC Thr Asn 1425  CAG GGC Gln Gly 1440  AAC AGC Asn Ser	Thr Val 1395  TAC CCC Tyr Pro 1410  CCC GTG Pro Val  ATC GAG Ile Glu  ATC ACC	768 816
GAC TGG ATC Asp Trp Ile 1380  CTG GAC ATC Leu Asp Ile  ATC CGC ACC Ile Arg Thr  CTG GAG AAC Leu Glu Asn 1430  GGC AGC ATC Gly Ser Ile	Arg Tyr Asn 138  GTG AGC CTG Val Ser Leu 1400  GTG AGC CAG Val Ser Gln 1415  TTC GAC GGC Phe Asp Gly  CGC AGC CCC Arg Ser Pro	CAG TTC Gln Phe 5  TTC CCC Phe Pro  CTG ACC Leu Thr  AGC TTC Ser Phe 1435  CAC CTG His Leu 1450  CGC GGC Arg Gly	Arg Arg  AAC TAC Asn Tyr 1405  CGC GAG Arg Glu 1420  CGC GGC Arg Gly  ATG GAC Met Asp  GAG TAC	GAG CTG Glu Leu 1390  GAC AGC Asp Ser  ATT TAC Ile Tyr  AGC GCC Ser Ala  ATC CTG Ile Leu 1455	ACC CTG Thr Leu  CGC ACC Arg Thr  ACC AAC Thr Asn 1425  CAG GGC Gln Gly 1440  AAC AGC Asn Ser  AGC GGC	Thr Val 1395  TAC CCC Tyr Pro 1410  CCC GTG Pro Val  ATC GAG Ile Glu  ATC ACC Ile Thr  CAC CAG	768 816 864

1480 1485 1490

				1480					1485	)				1490		
CTG Leu	TAC Tyr	GGC Gly	ACC Thr 1495	Met	GGC Gly	AAC Asn	GCT Ala	GCA Ala 1500	Pro	CAG Gln	CAG Gln	CGC Arg	ATC Ile 1505	Val	GCA Ala	1056
CAG Gln	CTG Leu	GGC Gly 1510	CAG Gln )	GGA Gly	GTG Val	TAC Tyr	CGC Arg 1515	Thr	CTG Leu	AGC Ser	AGC Ser	ACC Thr 1520	Leu	TAC Tyr	CGT Arg	1104
CGA Arg	CCT Pro 1525	Phe	AAC Asn	ATC Ile	GGC Gly	ATC Ile 1530	Asn	AAC Asn	CAG Gln	CAG Gln	CTG Leu 1535	Ser	GTG Val	CTG Leu	GAC Asp	1152
GGC Gly 1540	Thr	GAG Glu	TTC Phe	GCC Ala	TAC Tyr 1545	Gly	ACC Thr	AGC Ser	AGC Ser	AAC Asn 1550	Leu	CCC Pro	AGC Ser	GCC Ala	GTG Val 1555	1200
TAC Tyr	CGC Arg	AAG Lys	AGC Ser	GGC Gly 1560	Thr	GTG Val	GAC Asp	AGC Ser	CTG Leu 1565	Asp	GAG Glu	ATC Ile	CCC Pro	CCT Pro 1570	Gln	1248
AAC Asn	AAC Asn	AAC Asn	GTG Val 1575	Pro	CCT Pro	CGA Arg	CAG Gln	GGC Gly 1580	Phe	AGC Ser	CAC His	CGT Arg	CTG Leu 1585	Ser	CAC His	1296
Val	Ser	Met 1590		Arg	Ser	Gly	Phe 1595	Ser	Asn	Ser	Ser	Val 1600	Ser	·Ile	Ile	1344
Arg	Ala 1605	Pro	ATG Met	Phe	Ser	Trp 1610	Ile	His	Arg	Ser	Ala 161	Glu 5	Phe	Asn	Asn	1392
ATC Ile 1620	Ile	CCC Pro	AGC Ser	AGC Ser	CAG Gln 1625	Ile	ACC Thr	CAG Gln	ATC Ile	CCC Pro 1630	Leu	ACC Thr	AAG Lys	AGC Ser	ACC Thr 1635	1440
AAC Asn	CTG Leu	GGC Gly	AGC Ser	GGC Gly 1640	Thr	AGC Ser	GTG Val	GTG Val	AAG Lys 164	Gly	CCC Pro	GGC Gly	TTC Phe	ACC Thr 1650	Gly	1488
GGC Gly	GAC Asp	ATC Ile	CTG Leu 165	Arg	CGC Arg	ACC Thr	AGC Ser	CCC Pro 1660	Gly	CAG Gln	ATC Ile	AGC Ser	ACC Thr 166	Leu	CGC Arg	1536
GTG Val	AAC Asn	ATC Ile 167	ACC Thr 0	GCC Ala	CCC Pro	CTG Leu	AGC Ser 167	Gln	CGC Arg	TAC Tyr	CGC Arg	GTC Val 168	Arg	ATC Ile	CGC Arg	1584
TAC Tyr	GCC Ala 168	Ser	ACC Thr	ACC Thr	AAC Asn	CTG Leu 169	Gln	TTC Phe	CAC His	ACC Thr	AGC Ser 169	Ile	GAC Asp	GGC Gly	CGC Arg	1632
CCC Pro 170	Ile	AAC Asn	CAG Gln	GGC	AAC Asn 170	Phe	AGC Ser	GCC Ala	ACC Thr	ATG Met 171	Ser	AGC Ser	GGC Gly	AGC Ser	AAC Asn 1715	1680
CTG Leu	CAG Gln	AGC Ser	GGC Gly	AGC Ser 172	Phe	CGC Arg	ACC Thr	GTG Val	GGC Gly 172	Phe	ACC Thr	ACC Thr	CCC Pro	TTC Phe 173	Asn	1728

TTC AGC AAC GGC AG Phe Ser Asn Gly Se 1735	C AGC GTG TTC ACC r Ser Val Phe Thr 1740	CTG AGC GCC CAC GTG Leu Ser Ala His Val 1745	Phe Ash
AGC GGC AAC GAG GT Ser Gly Asn Glu Va 1750	G TAC ATC GAC CGC 1 Tyr Ile Asp Arg 1755	ATC GAG TTC GTG CCC Ile Glu Phe Val Pro 1760	GCC GAG 1824 Ala Glu
GTG ACC TTC GAG GO Val Thr Phe Glu Al 1765	C GAG TAC GAC CTG a Glu Tyr Asp Leu 1770	GAG AGG GCT CAG AAG Glu Arg Ala Gln Lys 1775	GCC GTG 1872 Ala Val
AAC GAG CTG TTC AC Asn Glu Leu Phe Th 1780	C AGC AGC AAC CAG r Ser Ser Asn Gln 1785	ATC GGC CTG AAG ACC Ile Gly Leu Lys Thr 1790	GAC GTG 1920 Asp Val 1795
Thr Asp Tyr His I	C GAT CAA GTA TCC e Asp Gln Val Ser	AAT TTA GTT GAG TGT Asn Leu Val Glu Cys 1805	TTA TCT 1968 Leu Ser 1810
GAT GAA TTT TGT CT Asp Glu Phe Cys Le 1815	G GAT GAA AAA AAA eu Asp Glu Lys Lys 1820	GAA TTG TCC GAG AAA Glu Leu Ser Glu Lys 1825	Val Lys
CAT GCG AAG CGA CT His Ala Lys Arg Le 1830	T AGT GAT GAG CGG eu Ser Asp Glu Arg 1835	AAT TTA CTT CAA GAT Asn Leu Leu Gln Asp 1840	CCA AAC 2064 Pro Asn
TTT AGA GGG ATC AMPhe Arg Gly Ile As	AT AGA CAA CTA GAC sn Arg Gln Leu Asp 1850	CGT GGC TGG AGA GGA Arg Gly Trp Arg Gly 1855	AGT ACG 2112 Ser Thr
GAT ATT ACC ATC CARS Ile Thr Ile G	AA GGA GGC GAT GAC In Gly Gly Asp Asp 1865	GTA TTC AAA GAG AAT Val Phe Lys Glu Asn 1870	TAC GTT 2160 Tyr Val 1875
Thr Leu Leu Gly T	CC TTC GAC GAG TGC or Phe Asp Glu Cys 880	TAC CCC ACC TAC CTG Tyr Pro Thr Tyr Leu 1885	TAC CAG 2208 Tyr Gln 1890
AAG ATC GAC GAG AG Lys Ile Asp Glu So 1895	GC AAG CTG AAG GCC er Lys Leu Lys Ala 190	TAC ACC CGC TAC CAG Tyr Thr Arg Tyr Gln 1905	Leu Arg
GGC TAC ATC GAG G Gly Tyr Ile Glu A 1910	AC AGC CAG GAC CTG sp Ser Gln Asp Leu 1915	GAA ATC TAC CTG ATC Glu Ile Tyr Leu Ile 1920	CGC TAC 2304 Arg Tyr
AAC GCC AAG CAC G Asn Ala Lys His G 1925	AG ACC GTG AAC GTG lu Thr Val Asn Val 1930	CCC GGC ACC GGC AGC Pro Gly Thr Gly Ser 1935	CTG TGG 2352 Leu Trp
CCC CTG AGC GCC C Pro Leu Ser Ala P 1940	CC AGC CCC ATC GGC ro Ser Pro Ile Gly 1945	AAG TGC GGG GAG CCG Lys Cys Gly Glu Pro 1950	AAT CGA 2400 Asn Arg 1955
Cys Ala Pro His L	rg GAG TGG AAC CCG eu Glu Trp Asn Pro 960	GAC CTA GAC TGC AGC Asp Leu Asp Cys Ser 1965	TGC AGG 2448 Cys Arg 1970

GAC Asp	GGG Gly	GAG Glu	AAG Lys 1975	Cys	GCC Ala	CAC His	CAC His	AGC Ser 1980	His	CAC His	TTC Phe	AGC Ser	CTG Leu 1985	Asp	ATC Ile	2496
GAC Asp	GTG Val	GGC Gly 1990	Cys	ACC Thr	GAC Asp	CTG Leu	AAC Asn 1995	Glu	GAC Asp	CTG Leu	GGC Gly	GTG Val 2000	Trp	GTG Val	ATC Ile	2544
TTC Phe	AAG Lys 2005	Ile	AAG Lys	ACC Thr	CAG Gln	GAC Asp 2010	Gly	CAC His	GCC Ala	CGC Arg	CTG Leu 2015	GGC Gly	AAT Asn	CTA Leu	GAA Glu	2592
TTT Phe 2020	Leu	GAA Glu	GAG Glu	AAA Lys	CCA Pro 2025	Leu	GTA Val	GGA Gly	GAA Glu	GCA Ala 2030	Leu	GCT Ala	CGT Arg	GTG Val	AAA Lys 2035	2640
AGA Arg	GCG Ala	GAG Glu	AAA Lys	AAA Lys 2040	Trp	AGA Arg	GAC Asp	AAA Lys	CGT Arg 2045	Glu	AAA Lys	TTG Leu	GAA Glu	TGG Trp 2050	Glu	2688
ACA Thr	AAT Asn	Ile	GTT Val 2055	Tyr	AAA Lys	GAG Glu	GCA Ala	AAA Lys 2060	Glu	TCT Ser	GTA Val	GAT Asp	GCT Ala 2065	Leu	TTT Phe	2736
GTA Val	AAC Asn	TCT Ser 2070	Gln	TAT Tyr	GAT Asp	AGA Arg	TTA Leu 2079	Gln	GCG Ala	GAT Asp	ACC Thr	AAC Asn 2080	Ile	GCG Ala	ATG Met	2784
ATT Ile	CAT His 2085	Ala	GCA Ala	GAT Asp	AAA Lys	CGC Arg 2090	Val	CAT His	AGC Ser	ATT Ile	CGA Arg 2095	GAA Glu 5	GCT Ala	TAT Tyr	CTG Leu	2832
CCT Pro 210	Glu	CTG Leu	TCT Ser	GTG Val	ATT Ile 2105	Pro	GGT Gly	GTC Val	AAT Asn	GCG Ala 211	Ala	ATT Ile	TTT Phe	GAA Glu	GAA Glu 2115	2880
TTA Leu	GAA Glu	GGG Gly	CGT Arg	ATT Ile 2120	Phe	ACT Thr	GCA Ala	TTC Phe	TCC Ser 212	Leu	TAT Tyr	GAT Asp	GCG Ala	AGA Arg 2130	Asn	2928
GTC Val	ATT Ile	AAA Lys	AAT Asn 213	Gly	GAT Asp	TTT Phe	AAT Asn	AAT Asn 2140	Gly	TTA Leu	TCC Ser	TGC Cys	TGG Trp 214	Asn	GTG Val	2976
AAA Lys	GGG Gly	CAT His 215	Val	GAT Asp	GTA Val	GAA Glu	GAA Glu 215	Gln	AAC Asn	AAC Asn	CAC His	CGT Arg 216	Ser	GTC Val	CTT Leu	3024
GTT Val	GTT Val 216	Pro	GAA Glu	TGG Trp	GAA Glu	GCA Ala 217	Glu	GTG Val	TCA Ser	CAA Gln	GAA Glu 217	GTT Val 5	CGT Arg	GTC Val	TGT Cys	3072
CCG Pro 218	Gly	CGT Arg	GGC Gly	TAT Tyr	ATC Ile 218	Leu	CGT Arg	GTC Val	ACA Thr	GCG Ala 219	Tyr	AAG Lys	GAG Glu	GGA Gly	TAT Tyr 2195	3120
GGA Gly	GAA Glu	GGT Gly	TGC Cys	GTA Val 220	Thr	ATT Ile	CAT His	GAG Glu	ATC Ile 220	Glu	AAC Asn	AAT Asn	ACA Thr	GAC Asp 221	Glu	3168
CTG	AAG	TTT	AGC	AAC	TGT	GTA	GAA	GAG	GAA	GTA	TAT	CCA	AAC	AAC	ACG	3216

a a a a a a a a a a a a a a a a a a a											
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2215 2220 2225											
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2230 2235 2240	3264										
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2245 2250 2255	3312										
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2260 2265 2270 2275	3360										
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT Asp Gly Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2280 2285 2290	3408										
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2295 2300 2305	3456										
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2310 2315 2320	3504										
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA  Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu  2325 2330 2335	3546										
(2) INFORMATION FOR SEQ ID NO:11:											
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 1181 amino acids  (B) TYPE: amino acid  (D) TOPOLOGY: linear											
(ii) MOLECULE TYPE: protein											
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:											
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10											
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30											
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45											
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60											
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80											

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 305 310 315

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His

420	425	430

Val	Ser	Met 435	Phe	Arg	Ser	Gly	Phe 440	Ser	Asn	Ser	Ser	Val 445	Ser	Ile	Ile
Arg	Ala 450	Pro	Met	Phe	Ser	Trp 455	Ile	His	Arg	Ser	Ala 460	Glu	Phe	Asn	Asn
Ile 465	Ile	Pro	Ser	Ser	Gln 470	Ile	Thr	Gln	Ile	Pro 475	Leu	Thr	Lys	Ser	Thr 480
Asn	Leu	Gly	Ser	Gly 485	Thr	Ser	Val	Val	Lys 490	Gly	Pro	Gly	Phe	Thr 495	Gly
Gly	Asp	Ile	Leu 500	Arg	Arg	Thr	Ser	Pro 505	Gly	Gln	Ile	Ser	Thr 510	Leu	Arg
Val	Asn	Ile 515	Thr	Ala	Pro	Leu	Ser 520	Gln	Arg	Tyr	Arg	Val 525	Arg	Ile	Arg
Tyr	Ala 530	Ser	Thr	Thr	Asn	Leu 535	Gln	Phe	His	Thr	Ser 540	Ile	Asp	Gly	Arg
Pro 545	Ile	Asn	Gln	Gly	Asn 550	Phe	Ser	Ala	Thr	Met 555	Ser	Ser	Gly	Ser	Asn 560
Leu	Gln	Ser	Gly	Ser 565	Phe	Arg	Thr	Val	Gly 570	Phe	Thr	Thr	Pro	Phe -575	Asn
Phe	Ser	Asn	Gly 580	Ser	Ser	Val	Phe	Thr 585	Leu	Ser	Ala	His	Val 590	Phe	Asn
Ser	Gly	Asn 595	Glu	Val	Tyr	Ile	Asp 600	Arg	Ile	Glu	Phe	Val 605	Pro	Ala	Glu
Val	Thr 610		Glu	Ala	Glu	Tyr 615		Leu	Glu	Arg	Ala 620	Gln	Lys	Ala	Val
Asn 625		Leu	Phe	Thr	Ser 630		Asn	Gln	Ile	Gly 635	Leu	Lys	Thr	Asp	Val 640
Thr	Asp	Tyr	His	Ile 645		Gln	Val	Ser	Asn 650	Leu	Val	Glu	Cys	Leu. 655	Ser
Asp	Glu	. Phe	Cys 660		Asp	Glu	Lys	Lys 665	Glu	Leu	Ser	Glu	Lys 670	Val	Lys
His	Ala	Lys 675	Arg	Leu	Ser	Asp	Glu 680	Arg	Asn	Leu	Leu	Gln 685	Asp	Pro	Asn
Phe	Arg 690		/ Ile	e Asn	a Arg	Gln 695		Asp	Arg	Gly	700	Arg	Gly	Ser	Thr
Asp 705		e Thr	: Ile	e Glr	Gly 710		Asp	Asp	Val	Phe 715	Lys	Glu	Asn	Tyr	Val 720
Thr	Lev	ı Lev	ı Gly	7 Thi 725		e Asp	Glu	ı Суs	730	Pro	Thr	Tyr	Leu	Tyr 735	Gln
Lys	s Ile	e Asp	o Glu		. Lys	. Lev	ı Lys	3 Ala	. Туг	Thr	Arg	Tyr	Gln 750	Leu	Arg

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 775 Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 810 805 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 825 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 840 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 855 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 870 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 885 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 955 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 985 Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 1005 1000 Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1020 Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1025 1035 Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1045 1050

1070

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr

1060

1065

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Th 1075 1080 1085	ır
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Se 1090 1095 1100	ir
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Th 1105 1110 1115 11	nr .20
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly As 1125 1130 1135	g.
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Ph 1140 1145 1150	ıe
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Th 1155 1160 1165	ır
Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu 1170 1175 1180	
(2) INFORMATION FOR SEQ ID NO:12:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 3546 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "Synthetic DNA"</pre>	
(iii) HYPOTHETICAL: NO	
<pre>(ix) FEATURE:</pre>	.d,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
ATG GAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CT Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Le 1185 1190 1195	rG 48 eu
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GG Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gl 1200 1205 1210	GC 96 Ly
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG ACC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Se 1215 1220 1225	GC 144 er
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG G	rC 192 le 245

TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Glu Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG  Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu  1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG  Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val  1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG  Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val  1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG	960

Ile	Tyr	Thr	Asp	Ala 149	His O	Arg	Gly	Glu	Tyr 149		Trp	Ser	Gly	His 150		
				Pro	GTC Val				Gly					Phe		1008
			Thr		GGC Gly			Ala					Ile			1056
CAG Gln	CTG Leu 1535	Gly	CAG Gln	GGA Gly	GTG Val	TAC Tyr 1540	Arg	ACC Thr	CTG Leu	AGC Ser	AGC Ser 1545	Thr	CTG Leu	TAC Tyr	CGT Arg	1104
	Pro				GGC Gly 1555	Ile					Leu					1152
					TAC Tyr )					Asn					Val	1200
				Gly	ACC Thr				Leu					Pro		1248
			Val		CCT Pro			Gly					Leu			1296
GTG Val	AGC Ser 1615	Met	TTC Phe	CGC Arg	AGT Ser	GGC Gly 1620	Phe	AGC Ser	AAC Asn	AGC Ser	AGC Ser 1625	Val	AGC Ser	ATC Ile	ATC Ile	1344
CGT Arg 1630	Ala	CCT Pro	ATG Met	TTC Phe	AGC Ser 1635	Trp	ATT Ile	CAC His	CGC Arg	AGT Ser 1640	Ala	GAG Glu	TTC Phe	AAC Asn	AAC Asn 1645	1392
ATC Ile	ATC Ile	CCC Pro	Ser	Ser	CAG Gln )	Ile	Thr	Gln	Ile	Pro	CTG Leu	ACC Thr	Lys	AGC Ser 1660	Thr	1440
AAC Asn	CTG Leu	GGC Gly	AGC Ser 1665	Gly	ACC Thr	AGC Ser	GTG Val	GTG Val 1670	Lys	GGC Gly	CCC Pro	GGC Gly	TTC Phe 1675	Thr	GGC Gly	1488
			Leu		CGC Arg			Pro					Thr			1536
GTG Val	AAC Asn 1695	Ile	ACC Thr	GCC Ala	CCC Pro	CTG Leu 1700	Ser	CAG Gln	CGC Arg	TAC Tyr	CGC Arg 1705	Val	CGC Arg	ATC Ile	CGC Arg	1584
TAC Tyr 1710	Ala	AGC Ser	ACC Thr	ACC Thr	AAC Asn 1715	Leu	CAG Gln	TTC Phe	CAC His	ACC Thr 1720	Ser	ATC Ile	GAC Asp	GGC Gly	CGC Arg 1725	1632
CCC Pro	ATC Ile	AAC Asn	CAG Gln	GGC Gly	AAC Asn	TTC Phe	AGC Ser	GCC Ala	ACC Thr	ATG Met	AGC Ser	AGC Ser	GGC Gly	AGC Ser	AAC Asn	1680

1730 1735 1740 CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC 1728 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 1745 1750 TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC 1776 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 1765 AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG 1824 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1775 1780 GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG 1872 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1795 1800 AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG 1920 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 1810 1815 ACC GAC TAC- CAC ATC GAT CAG GTG AGC AAC CTG GTG GAG TGC TTA AGC 1968 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 1825 1830 GAC GAG TTC TGC CTG GAC GAG AAG GAG GAG CTG AGC GAG AAG GTG AAG 2016 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 1845 CAC GCC AAG CGC CTG AGC GAC GAG CGC AAC CTG CTG CAG GAC CCC AAC 2064 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 1855 1860 TTC CGC GGC ATC AAC CGC CAG CTG GAC CGC GGC TGG CGA GGC AGC ACC 2112 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr GAT ATC ACC ATC CAG GGC GGC GAC GAC GTG TTC AAG GAG AAC TAC GTG 2160 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 1895 ACC CTG CTG GGC ACC TTC GAC GAG TGC TAC CCC ACC TAC CTG TAC CAG 2208 Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 1910 AAG ATC GAC GAG AGC AAG CTG AAG GCC TAC ACC CGC TAC CAG CTG CGC 2256 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 1925 GGC TAC ATC GAG GAC AGC CAG GAC CTG GAA ATC TAC CTG ATC CGC TAC 2304 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 1935 1940 AAC GCC AAG CAC GAG ACC GTG AAC GTG CCC GGC ACC GGC AGC CTG TGG 2352 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 1955 1960 CCC CTG AGC GCC CCC AGC CCC ATC GGC AAG TGC GGG GAG CCG AAT CGA 2400 Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 1970 1975

TGC Cys	GCT Ala	CCG Pro	CAC His 198	Leu	GAG Glu	TGG Trp	AAC Asn	CCG Pro 199	Asp	CTA Leu	GAC Asp	TGC Cys	AGC Ser 199	Cys	AGG Arg	2448
GAC Asp	GGG Gly	GAG Glu 200	Lys	TGC Cys	GCC Ala	CAC His	CAC His 200	Ser	CAC His	CAC His	TTC Phe	AGC Ser 201	Leu	GAC Asp	ATC	2496
GAC Asp	GTG Val 201	Gly	TGC Cys	ACC Thr	GAC Asp	CTG Leu 202	Asn	GAG Glu	GAC Asp	CTG Leu	GGC Gly 202	Val	TGG Trp	GTG Val	ATC Ile	2544
TTC Phe 203	Lys	ATC Ile	AAG Lys	ACC Thr	CAG Gln 203	Asp	GGC Gly	CAC His	GCC Ala	CGC Arg 204	Leu	GGC Gly	AAT Asn	CTA Leu	GAA Glu 2045	2592
TTT Phe	CTC Leu	GAA Glu	GAG Glu	AAA Lys 205	Pro	TTA Leu	GTA Val	GGA Gly	GAA Glu 205	Ala	CTA Leu	GCT Ala	CGT Arg	GTG Val 206	_	2640
AGA Arg	GCG Ala	GAG Glu	AAA Lys 206	Lys	TGG Trp	AGA Arg	GAC Asp	AAA Lys 207	CGT Arg 0	GAA Glu	AAA Lys	TTG Leu	GAA Glu 207	Trp	GAA Glu	2688
ACA Thr	AAT Asn	ATT Ile 2080	Val	TAT Tyr	AAA Lys	GAG Glu	GCA Ala 2085	Lys	GAA Glu	TCT Ser	GTA Val	GAT Asp 209	Ala	TTA Leu	TTT Phe	2736
GTA Val	AAC Asn 209	Ser	CAA Gln	TAT Tyr	GAT Asp	AGA Arg 2100	Leu	CAA Gln	GCG Ala	GAT Asp	ACC Thr 210	Asn	ATC Ile	GCG Ala	ATG Met	2784
ATT Ile 2110	His	GCG Ala	GCA Ala	GAT Asp	AAA Lys 211	Arg	GTT Val	CAT His	AGC Ser	ATT Ile 2120	Arg	GAA Glu	GCT Ala	TAT Tyr	CTG Leu 2125	2832
CCT Pro	GAG Glu	CTG Leu	TCT Ser	GTG Val 2130	Ile	CCG Pro	GGT Gly	GTC Val	AAT Asn 2135	Ala	GCT Ala	ATT Ile	TTT Phe	GAA Glu 2140	Glu	2880
TTA Leu	GAA Glu	GGG Gly	CGT Arg 2145	Ile	TTC Phe	ACT Thr	GCA Ala	TTC Phe 2150	TCC Ser	CTA Leu	TAT Tyr	GAT Asp	GCG Ala 215	Arg	AAT Asn	2928
GTC Val	ATT Ile	AAA Lys 2160	Asn	GGT Gly	GAT Asp	TTT Phe	AAT Asn 2165	Asn	GGC Gly	TTA Leu	TCC Ser	TGC Cys 2170	Trp	AAC Asn	GTG Val	2976
AAA Lys	GGG Gly 2175	His	GTA Val	GAT Asp	GTA Val	GAA Glu 2180	Glu	CAA Gln	AAC Asn	AAC Asn	CAC His 2185	Arg	TCG Ser	GTC Val	CTT Leu	3024
GTT Val 2190	Val	CCG Pro	GAA Glu	TGG Trp	GAA Glu 2195	Ala	GAA Glu	GTG Val	TCA Ser	CAA Gln 2200	Glu	GTT Val	CGT Arg	GTC Val	TGT Cys 2205	3072
CCG Pro	GGT Gly	CGT Arg	GGC Gly	TAT Tyr 2210	Ile	CTT Leu	CGT Arg	GTC Val	ACA Thr 2215	Ala	TAC Tyr	AAG Lys	GAG Glu	GGA Gly 2220	Tyr	3120

GGA GAZ Gly Glu	GGT Gly	TGC Cys 222	Val	ACC Thr	ATT Ile	CAT His	GAG Glu 223	Ile	GAG Glu	AAC Asn	AAT Asn	ACA Thr 223	Asp	GAA Glu	3168
CTG AAC Leu Lys	TTT Phe 224	Ser	AAC Asn	TGT Cys	GTA Val	GAA Glu 2245	Glu	GAA Glu	GTA Val	TAT Tyr	CCA Pro 225	Asn	AAC Asn	ACG Thr	3216
GTA ACC Val Thr 225	. Cys	AAT Asn	GAT Asp	TAT Tyr	ACT Thr 2260	Ala	ACT Thr	CAA Gln	GAA Glu	GAA Glu 2265	Tyr	GAG Glu	GGT Gly	ACG Thr	3264
TAC ACT Tyr Thr 2270	TCT Ser	CGT Arg	AAT Asn	CGA Arg 2275	Gly	TAT Tyr	GAC Asp	GGA Gly	GCC Ala 2280	Tyr	GAA Glu	AGC Ser	AAT Asn	TCT Ser 2285	3312
TCT GTA Ser Val				Tyr					Glu					Thr	3360
GAT GGA Asp Gly	Arg	AGA Arg 2305	Asp	AAT Asn	CCT Pro	TGT Cys	GAA Glu 2310	Ser	AAC Asn	AGA Arg	GGA Gly	TAT Tyr 2315	Gly	GAT Asp	3408
TAC ACA Tyr Thr	CCA Pro 2320	Leu	CCA Pro	GCT Ala	GGC Gly	TAT Tyr 2325	Val	ACA Thr	AAA Lys	GAA Glu	TTA Leu 2330	Glu	TAC Tyr	TTC Phe	3456
CCA GAA Pro Glu 233	Thr	GAT Asp	AAG Lys	Val	TGG Trp 2340	Ile	GAG Glu	ATC Ile	GGA Gly	GAA Glu 2345	Thr	GAA Glu	GGA Gly	ACA Thr	3504
TTC ATC Phe Ile 2350	GTG Val	GAC Asp	AGC Ser	GTG Val 2355	Glu	TTA Leu	CTT Leu	CTT Leu	ATG Met 2360	Glu	GAA Glu	TAA			3546
/2\ TNE	∩рмлп	1T/37	EOR	CEO	TD 33	·0 12									

### (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1181 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu

1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile

65					70					75					80
Glu	Gln	Leu	Ile	Asn 85	Gln	Arg	Ile	Glu	Glu 90	Phe	Ala	Arg	Asn	Gln 95	Ala
Ile	Ser	Arg	Leu 100	Glu	Gly	Leu	Ser	Asn 105	Leu	Tyr	Gln	Ile	Туг 110	Ala	Glu
Ser	Phe	Arg 115	Glu	Trp	Glu	Ala	Asp 120	Pro	Thr	Asn	Pro	Ala 125	Leu	Arg	Glu
Glu	Met 130	Arg	Ile	Gln	Phe	Asn 135	Asp	Met	Asn	Ser	Ala 140	Leu	Thr	Thr	Ala
Ile 145	Pro	Leu	Phe	Ala	Val 150	Gln	Asn	Tyr	Gln	Val 155	Pro	Leu	Leu	Ser	Val 160
Tyr	Val	Gln	Ala	Ala 165	Asn	Leu	His	Leu	Ser 170	Val	Leu	Arg	Asp	Val 175	Ser
Val	Phe	Gly	Gln 180	Arg	Trp	Gly	Phe	Asp 185	Ala	Ala	Thr	Ile	Asn 190	Ser	Arg
Tyr	Asn	Asp 195	Leu	Thr	Arg	Leu	Ile 200	Gly	Asn	Tyr	Thr	Asp 205	His	Ala	Val
Arg	Trp 210	Tyr	Asn	Thr	Gly	Leu 215	Glu	Arg	Val	Trp	Gly 220	Pro	Asp		Arg
Asp 225	Trp	Ile	Arg	Tyr	Asn 230	Gln	Phe	Arg	Arg	Glu 235	Leu	Thr	Leu	Thr	Val 240
Leu	Asp	Ile	Val	Ser 245	Leu	Phe	Pro	Asn	Tyr 250	Asp	Ser	Arg	Thr	Tyr 255	Pro
Ile	Arg	Thr	Val 260	Ser	Gln	Leu	Thr	Arg 265	Glu	Ile	Tyr	Thr	Asn 270	Pro	Val
		275	Phe		_		280		_			285	_		
Gly	Ser 290	Ile	Arg	Ser	Pro	His 295	Leu	Met	Asp	Ile	Leu 300	Asn	Ser	Ile	Thr
11e 305	Tyr	Thr	Asp	Ala	His 310	Arg	Gly	Glu	Tyr	Tyr 315	Trp	Ser	Gly	His	Gln 320
Ile	Met	Ala	Ser	Pro 325	Val	Gly	Phe	Ser	Gly 330	Pro	Glu	Phe	Thr	Phe 335	Pro
Leu	Tyr	Gly	Thr 340	Met	Gly	Asn	Ala	Ala 345	Pro	Gln	Gln	Arg	Ile 350	Val	Ala
Gln	Leu	Gly 355	Gln	Gly	Val	Tyr	Arg 360	Thr	Leu	Ser	Ser	Thr 365	Leu	Tyr	Arg
Arg	Pro 370	Phe	Asn	Ile	Gly	Ile 375	Asn	Asn	Gln	Gln	Leu 380	Ser	Val	Leu	Asp
Gly 385	Thr	Glu	Phe	Ala	Tyr 390	Gly	Thr	Ser	Ser	Asn 395	Leu	Pro	Ser	Ala	Val 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 425 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 455 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 475 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 505 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 535 540 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 550 555 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 565 570 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 585 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 600 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 635 630 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 645 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 665 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 675 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 695 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val

715

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 725

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 770 780

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 900 905 910

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 995 1000 1005

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu

1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr

Val Thr Cys Asn Asp Tyr Thr Ala Thr Glu Glu Tyr Glu Gly Thr 1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1105 1110 1115 1120

Asp Gly Arg Asp Asp Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu 1170 1175 1180

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 3546 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: other nucleic acid
    - (A) DESCRIPTION: /desc = "Synthetic DNA"
  - (iii) HYPOTHETICAL: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..3543
  - (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)" /note= "Disclosed in Figure 13 as contained in pCIB5513."
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
- ATG GAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG

  Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu

  1185

  1190

  1195
- AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC
  Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
  1200 1205 1210
- TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC

  Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser

  1215

  1220

  1225

GAG TTC GTG CCC GGC GCC Glu Phe Val Pro Gly Ala 1230 1235	Gly Phe Val Leu Gly	Leu Val Asp Ile Ile	192
TGG GGC ATC TTC GGC CCC Trp Gly Ile Phe Gly Pro 1250			240
GAG CAG CTG ATC AAC CAG Glu Gln Leu Ile Asn Gln 1265			288
ATC AGC CGC CTG GAG GGC Ile Ser Arg Leu Glu Gly 1280			336
AGC TTC CGC GAG TGG GAG Ser Phe Arg Glu Trp Glu 1295			384
GAG ATG CGC ATC CAG TTC Glu Met Arg-Ile Gln Phe 1310 1315	Asn Asp Met Asn Ser	Ala Leu Thr Thr Ala	432
ATC CCC CTG TTC GCC GTG Ile Pro Leu Phe Ala Val 1330			480
TAC GTG CAG GCC GCC AAC Tyr Val Gln Ala Ala Asn 1345			528
GTG TTC GGC CAG CGC TGG Val Phe Gly Gln Arg Trp 1360			576
TAC AAC GAC CTG ACC CGC Tyr Asn Asp Leu Thr Arg 1375			624
CGC TGG TAC AAC ACC GGC Arg Trp Tyr Asn Thr Gly 1390	Leu Glu Arg Val Trp	Gly Pro Asp Ser Arg	672
GAC TGG ATC AGG TAC AAC Asp Trp Ile Arg Tyr Asn 1410			720
CTG GAC ATC GTG AGC CTG Leu Asp Ile Val Ser Leu 1425			768
ATC CGC ACC GTG AGC CAG Ile Arg Thr Val Ser Gln 1440			816
CTG GAG AAC TTC GAC GGC Leu Glu Asn Phe Asp Gly 1455			864

GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1490 1495 1500	960
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1505 1510 1515	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1520 1530	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1535 1540 1545	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1550 1565	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1570 1580	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1585 1590 1595	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1600 1605 1610	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1615 1620 1625	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1630 1635 1640 1645	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1650 1655 1660	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1665 1670 1675	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1680 1685 1690	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1695 1700 1705	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC	1632

Tyr Ala Ser Thr 1710	Thr Asn Leu Gli 1715	n Phe His Thr Se 1720	r Ile Asp Gly	Arg 1725
CCC ATC AAC CAG Pro Ile Asn Gln				Asn
CTG CAG AGC GGC Leu Gln Ser Gly 1745	Ser Phe Arg Th			
TTC AGC AAC GGC Phe Ser Asn Gly 1760		e Thr Leu Ser Al		
AGC GGC AAC GAG Ser Gly Asn Glu 1775			e Val Pro Ala	
GTG ACC TTC GAG Val Thr Phe Glu 1790				
AAC GAG CTG TTC Asn Glu Leu Phe				Val
ACC GAC TAC CAC Thr Asp Tyr His 1825	Ile Asp Gln Va			
GAC GAG TTC TGC Asp Glu Phe Cys 1840		s Lys Glu Leu Se		
CAC GCC AAG CGC His Ala Lys Arg 1855		ı Arg Asn Leu Le		
TTC CGC GGC ATC Phe Arg Gly Ile 1870		G GAC CGC GGC TG 1 Asp Arg Gly Tr 1880		
GAT ATC ACC ATC Asp Ile Thr Ile		C GAC GTG TTC AA		0.1.60
	1890			Val
ACC CTG CAG GGC Thr Leu Gln Gly 190	ACC TTC GAC GA Thr Phe Asp Gl	p Asp Val Phe Ly 1895 G TGC TAC CCC AC	s Glu Asn Tyr 1900 C TAC CTG TAC	Val ) CAG 2208
Thr Leu Gln Gly 1909 CCG ATC GAC GAG	ACC TTC GAC GAG Thr Phe Asp Glo  AGC AAG CTG AAG	Asp Val Phe Ly 1895  G TGC TAC CCC AC Cys Tyr Pro Th 1910  G GCC TAC ACC CG Ala Tyr Thr Ar	S Glu Asn Tyr 1900 C TAC CTG TAC TY Leu Tyr 1915 C TAC CAG CTG	Val CAG 2208 Gln CGC 2256
Thr Leu Gln Gly 1909  CCG ATC GAC GAG Pro Ile Asp Glu 1920  GGC TAC ATC GAG	ACC TTC GAC GAC Thr Phe Asp Glo  AGC AAG CTG AAC Ser Lys Leu Ly  GAC AGC CAG GAC	Asp Val Phe Ly 1895  G TGC TAC CCC AC Cys Tyr Pro Th 1910  G GCC TAC ACC CG A Ala Tyr Thr Ar C CTG GAA ATC TA C Leu Glu Ile Ty	C TAC CTG TAC TYT Leu TYT 1915 C TAC CAG CTG TYT Gln Leu 1930 C CTG ATC CGC	CAG 2208 Gln 2256 Arg 2304

1950	1955	1960	1965
CCC CTG AGC GCC CCC Pro Leu Ser Ala Pro 1970	AGC CCC ATC GGC AAG Ser Pro Ile Gly Lys ) 1975	Cys Gly Glu Pro Asii	ALG
TGC GCT CCG CAC CTG Cys Ala Pro His Leu 1985	GAG TGG AAC CCG GAC Glu Trp Asn Pro Asp 1990	CTA GAC TGC AGC TGC Leu Asp Cys Ser Cys 1995	AGG 2448 Arg
GAC GGG GAG AAG TGC Asp Gly Glu Lys Cys 2000	GCC CAC CAC AGC CAC Ala His His Ser His 2005	CAC TTC AGC CTG GAC His Phe Ser Leu Asp 2010	ATC 2496 Ile
GAC GTG GGC TGC ACC Asp Val Gly Cys Thr 2015	GAC CTG AAC GAG GAC Asp Leu Asn Glu Asp 2020	CTG GGC GTG TGG GTG Leu Gly Val Trp Val 2025	ATC 2544 Ile
TTC AAG ATC AAG ACC Phe Lys Ile Lys Thr 2030	CAG GAC GGC CAC GCC Gln Asp Gly His Ala 2035	CGC CTG GGC AAT CTA Arg Leu Gly Asn Leu 2040	GAG 2592 Glu 2045
TTC CTG GAG GAG AAG Phe Leu Glu Glu Lys 205	CCC CTG GTG GGC GAG Pro Leu Val Gly Glu 0 205	Ala Leu Ala Arg Vai	. Lys
CGC GCC GAG AAG AAG Arg Ala Glu Lys Lys 2065	TGG CGC GAC AAG CGC Trp Arg Asp Lys Arg 2070	GAG AAG CTG GAG TGG Glu Lys Leu Glu Trg 2075	G GAG 2688 O Glu
ACC AAC ATC GTG TAC Thr Asn Ile Val Tyr 2080	: AAG GAG GCC AAG GAG : Lys Glu Ala Lys Glu 2085	G AGC GTG GAC GCC CTG n Ser Val Asp Ala Leu 2090	TTC 2736
GTG AAC AGC CAG TAC Val Asn Ser Gln Tyr 2095	GAC CGC CTG CAG GCC Asp Arg Leu Gln Ala 2100	C GAC ACC AAC ATC GCC A Asp Thr Asn Ile Ala 2105	C ATG 2784 a Met
ATC CAC GCC GCC GAC Ile His Ala Ala Asg 2110	C AAG CGC GTG CAC AGC D Lys Arg Val His Ser 2115	C ATT CGC GAG GCC TAC r Ile Arg Glu Ala Ty 2120	C CTG 2832 c Leu 2125
CCC GAG CTG AGC GTG Pro Glu Leu Ser Val 213	G ATC CCC GGC GTG AAC l Ile Pro Gly Val Ass 30 21	n Ala Ala Ile Phe Gi	u Giu
CTC GAG GGC CGC ATC Leu Glu Gly Arg Ile 2145	C TTC ACC GCC TTC AGG e Phe Thr Ala Phe Se: 2150	C CTG TAC GAC GCC CGC r Leu Tyr Asp Ala Ar 2155	C AAC 2928 g Asn
GTG ATC AAG AAC GG Val Ile Lys Asn Gl 2160	C GAC TTC AAC AAC GG y Asp Phe Asn Asn Gl 2165	C CTG AGC TGC TGG AA y Leu Ser Cys Trp As: 2170	C GTG 2976 n Val
AAG GGC CAC GTG GA Lys Gly His Val As 2175	C GTG GAG GAG CAG AA p Val Glu Glu Gln As 2180	C AAC CAC CGC AGC GT n Asn His Arg Ser Va 2185	G CTG 3024 1 Leu
GTG GTG CCC GAG TG Val Val Pro Glu Tr 2190	G GAG GCC GAG GTG AG p Glu Ala Glu Val Se 2195	C CAG GAG GTG CGC GT r Gln Glu Val Arg Va 2200	G TGC 3072 1 Cys 2205

CCC GGC Pro Gly	CGC Arg	Gly	TAC Tyr 2210	Ile	CTG Leu	CGC Arg	vaı	ACC Thr 2215	ATG	TAC Tyr	AAG Lys	GAG Glu	GGC Gly 2220	-2-	3120
GGC GAG Gly Glu	GGC Gly	TGC Cys 2225	Val	ACC Thr	ATC Ile	CAC His	GAG Glu 2230	TTE	GAG Glu	AAC Asn	AAC Asn	ACC Thr 2235	1100	GAG Glu	3168
CTC AAG	TTC Phe 2240	Ser	AAC Asn	TGC Cys	GTG Val	GAG Glu 2245	GIU	GAG Glu	GTT Val	TAC Tyr	CCC Pro 2250	ASII	AAC Asn	ACC Thr	3216
GTG ACC Val Thr 225	Cys	AAC Asn	GAC Asp	TAC Tyr	ACC Thr 226	Ala	ACC Thr	CAG Gln	GAG Glu	GAG Glu 226	TAT	GAA Glu	GGC Gly	ACC Thr	3264
TAC ACC Tyr Thi 2270	TCT Ser	CGC Arg	AAC Asn	AGG Arg 227	GIY	TAC Tyr	GAC Asp	GGC Gly	GCC Ala 228	IAT	GAG Glu	TCC Ser	AAC Asn	AGC Ser 2285	3312
TCC GTG Ser Va	G CCA L Pro	GCC Ala	GAC Asp 229	Tyr	GCC Ala	AGC Ser	GCC Ala	TAC Tyr 229	GIU	GAG Glu	AAA Lys	GCC Ala	TAC Tyr 230		3360
GAC GG Asp Gl	r AGA y Arg	CGC Arg 230	Asp	AAC Asn	CCA Pro	TGT Cys	GAG Glu 231	Ser	AAC Asn	AGA Arg	GGC Gly	TAC Tyr 231	0-7	GAC Asp	3408
TAC AC	C CCC r Pro 232	Leu	CCC Pro	GCT Ala	GGA Gly	TAC Tyr 232	vai	ACC Thr	AAG Lys	GAG Glu	CTG Leu 233	. Gra	TAC Tyr	TTC Phe	3456
CCC GA Pro G1 23	G ACC u Thr 35	GAC Asp	AAG Lys	GTG Val	TGG Trp 234	Ile	GAG Glu	ATT	GGC Gly	GAG Glu 234	1 1111	GAG Glu	GGC Gly	ACC Thr	3504
TTC AT Phe Il 2350	C GTG e Val	GAC Asp	AGC Ser	GTC Val 235	. GIU	CTC Lev	CTC	CTC Lev	ı met	GAC Glu	G GAC	TAG	<b>;</b>		3546

### (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1181 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 105 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 135 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 155 150 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 170 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 185 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 215 Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 265 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 280 Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 295 290 Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 345 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg

360

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 375 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 395 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 425 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 455 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 475 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 485 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 520 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 555 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 585 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 650 645 Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr

69	90				6	595					700				
Asp I:	le :	Thr	Ile	Gln (	Gly (	Gly	Asp	Asp	Val	Phe 715	Lys	Glu .	Asn '	Tyr	Val 720
Thr L	eu (	Gln	Gly	Thr :	Phe i	Asp	Glu	Cys	Tyr 730	Pro	Thr	Tyr	Leu	Tyr 735	Gln
Pro I	le 2	Asp	Glu 740	Ser	Lys :	Leu	Lys	Ala 745	Tyr	Thr	Arg	Tyr	Gln 750	Leu	Arg
Gly T	уr	Ile 755	Glu	Asp	Ser	Gln	Asp 760	Leu	Glu	Ile	Tyr	Leu 765	Ile	Arg	Tyr
Asn A	la 70	Lys	His	Glu	Thr	Val 775	Asn	Val	Pro	Gly	Thr 780	Gly	Ser	Leu	Trp
Pro I 785	eu	Ser	Ala	Pro	Ser 790	Pro	Ile	Gly	Lys	Cys 795	Gly	Glu	Pro	Asn	Arg 800
Cys A	Ala	Pro	His	Leu 805	Glu	Trp	Asn	Pro	Asp 810	Leu	Asp	Cys	Ser	Cys 815	Arg
Asp (	Gly	Glu	Lys 820	Cys	Ala	His	His	Ser 825	His	His	Phe	Ser	Leu 830	Asp	Ile
Asp \	Val	Gly 835	Cys	Thr	Asp	Leu	Asn 840	Glu	. Asp	Leu	Gly	Val 845	Trp	Val	Ile
Phe 1	Lys 850	Ile	Lys	Thr	Gln	Asp 855	Gly	His	s Ala	a Arg	Leu 860	Gly	Asn	Leu	Glu
Phe	Leu	Glu	Glu	Lys	Pro 870	Leu	ı Val	. Gly	/ Glu	a Ala 875	Leu 5	Ala	Arg	Val	Lys 880
Arg	Ala	Glu	Lys	Lys 885	Trp	Arg	J Asp	) Lys	89	g Glu O	ı Lys	Leu	Glu	Trp 895	Glu
Thr	Asn	Ile	• Val	Tyr	Lys	Glu	ı Ala	a Ly:	s Gl	u Se:	r Val	Asp	Ala 910	Leu	Phe
Val	Asn	Ser 915	Glr	ı Tyr	Asp	Arg	g Let 92	u Gl: 0	n Al	a As	p Thr	925	ıle	Ala	Met
Ile	His		a Ala	a Asp	Lys	93	g Va	l Hi	s Se	r Il	e Arg 940	g Glu )	ı Ala	а Туі	Leu
Pro 945	Glu	ı Leı	ı Se	r Val	1 Ile 950	e Pr	o Gl	y Va	l As	n Al 95	a Ala 5	a Ile	e Phe	e Glu	1 Glu 960
Leu	Glu	ı Gl	y Ar	g Ile 96!	e Phe	e Th	r Al	a Ph	e Se 97	r Le '0	u Ty	r Ası	o Ala	a Arg	g Asn 5
Val	Ile	e Ly	s As 98	n Gly 0	y Asj	o Ph	e As	n As 98	n Gl	у Г€	eu Se	r Cy	s Tr	p Asi 0	n Val
Lys	Gl	y Hi 99		.1 As	p Va	1 G1	u Gl 10	.u G] 000	ln As	sn As	sn Hi	s Ar 10	g Se 05	r Va	l Leu
Val	Va 10	l Pr 10	o Gl	u Tr	p Gl	u Al 10	.a Gl )15	Lu Va	al Se	er G	ln Gl 10	u Va 20	l Ar	g Va	l Cys

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1025 1030 1035 1040										
Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1045 1050 1055										
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1060 1065 1070										
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1075 1080 1085										
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1090 1095 1100										
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1105 1110 1115 1120										
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1125 1130 1135										
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1140 1145 1150										
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1155 1160 1165										
Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu 1170 1175 1180										
(2) INFORMATION FOR SEQ ID NO:16:										
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 3547 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear										
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "Synthetic DNA"</pre>										
(iii) HYPOTHETICAL: NO										
<pre>(ix) FEATURE:</pre>										
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:										
ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1185 1190 1195	48									
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	96									

1210 1205 1200 TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC 144 Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 1220 192 Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1240 1235 TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC 240 Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1255 1250 GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC 288 Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1270 ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG 336 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1285 AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG 384 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1300 GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC 432 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1320 1315 ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG 480 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1335 1330 TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC 528 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1350 1345 GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC 576 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1365 TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG 624 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1380 CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC 672

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1395 GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG 720 Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1415 1410 CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC 768 Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1430 ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG 816 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445

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CTG GAG AAC TTC GAC GGC AGC Leu Glu Asn Phe Asp Gly Sec 1455	r Phe Arg Gly	AGC GCC CAG GGC Ser Ala Gln Gly 1465	ATC GAG 864 Ile Glu
GGC AGC ATC CGC AGC CCC CAG Gly Ser Ile Arg Ser Pro His 1470 1475	s Leu Met Asp	ATC CTG AAC AGC Ile Leu Asn Ser 1480	ATC ACC 912 Ile Thr 1485
ATC TAC ACC GAC GCC CAC CG Ile Tyr Thr Asp Ala His Ar 1490	C GGC GAG TAC g Gly Glu Tyr 1495	Tyr Trp Ser Gry	CAC CAG 960 His Gln 1500
ATC ATG GCC AGC CCC GTC GG Ile Met Ala Ser Pro Val Gl 1505	C TTC AGC GGC y Phe Ser Gly 1510	CCC GAG TTC ACC Pro Glu Phe Thr 151	File 110
CTG TAC GGC ACC ATG GGC AA Leu Tyr Gly Thr Met Gly As 1520	C GCT GCA CCT n Ala Ala Pro 1525	CAG CAG CGC ATC Gln Gln Arg Ile 1530	GTG GCA 1056 Val Ala
CAG CTG GGC CAG GGA GTG TA Gln Leu Gly Gln Gly Val Ty 1535	C CGC ACC CTG r Arg Thr Leu 40	AGC AGC ACC CTG Ser Ser Thr Leu 1545	TAC CGT 1104 Tyr Arg
CGA CCT TTC AAC ATC GGC AT Arg Pro Phe Asn Ile Gly Il 1550 1555	C AAC AAC CAG e Asn Asn Gln	CAG CTG AGC GTG Gln Leu Ser Val 1560	CTG GAC 1152 Leu Asp . 1565
GGC ACC GAG TTC GCC TAC GG Gly Thr Glu Phe Ala Tyr Gl 1570	CC ACC AGC AGC Ly Thr Ser Ser 157	Ash Leu Plo Ser	GCC GTG 1200 Ala Val 1580
TAC CGC AAG AGC GGC ACC GT Tyr Arg Lys Ser Gly Thr Va 1585	TG GAC AGC CTG al Asp Ser Leu 1590	GAC GAG ATC CCC Asp Glu Ile Pro 159	110 0111
AAC AAC AAC GTG CCA CCT CC Asn Asn Asn Val Pro Pro A 1600	GA CAG GGC TTC rg Gln Gly Phe 1605	AGC CAC CGT CTG Ser His Arg Leu 1610	AGC CAC 1296 Ser His
GTG AGC ATG TTC CGC AGT GC Val Ser Met Phe Arg Ser G 1615	GC TTC AGC AAC ly Phe Ser Asn 620	AGC AGC GTG AGC Ser Ser Val Ser 1625	ATC ATC 1344 Tile Ile
CGT GCA CCT ATG TTC AGC TO Arg Ala Pro Met Phe Ser To 1630	GG ATT CAC CGC rp Ile His Arg	AGT GCC GAG TTC Ser Ala Glu Pho 1640	2 AAC AAC 1392 2 Asn Asn 1645
ATC ATC CCC AGC AGC CAG A Ile Ile Pro Ser Ser Gln I 1650	TC ACC CAG ATC le Thr Gln Ile 165	Pro Leu Thi Ly	G AGC ACC 1440 S Ser Thr 1660
AAC CTG GGC AGC GGC ACC A Asn Leu Gly Ser Gly Thr S 1665	GC GTG GTG AAG er Val Val Lys 1670	GGC CCC GGC TTG Gly Pro Gly Pho 16	- Int Gry
GGC GAC ATC CTG CGC CGC A Gly Asp Ile Leu Arg Arg T 1680	CC AGC CCC GGC hr Ser Pro Gly 1685	CAG ATC AGC ACC Gln Ile Ser Th 1690	C CTG CGC 1536 r Leu Arg

GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1695	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 1710 1715 1720 1725	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 1730 1735 1740	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 1745 1750 1755	1728
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC  Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn  1760 1770	1776
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1775 1780 1785	1824
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1790 1800 1805	1872
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 1810 1815	1920
ACC GAC TAC CAC ATC GAT CAA GTA TCC AAT TTA GTT GAG TGT TTA TCT Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 1825 1830 1835	1968
GAT GAA TTT TGT CTG GAT GAA AAA AAA GAA TTG TCC GAG AAA GTC AAA Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 1840 1845 1850	2016
CAT GCG AAG CGA CTT AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 1855 1860 1865	2064
TTT AGA GGG ATC AAT AGA CAA CTA GAC CGT GGC TGG AGA GGA AGT ACG Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 1870 1885	2112
GAT ATT ACC ATC CAA GGA GGC GAT GAC GTA TTC AAA GAG AAT TAC GTT Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 1890	2160
ACG CTA TTG GGT ACC TTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAA Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 1905 1910 1915	2208
AAA ATA GAT GAG TCG AAA TTA AAA GCC TAT ACC CGT TAC CAA TTA AGA Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 1920 1925 1930	2256
GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC TAT TTA ATT CGC TAC	2304

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 1935 1940 1945	
AAT GCC AAA CAC GAA ACA GTA AAT GTG CCA GGT ACG GGT TCC TTA TGG Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 1950 1960 1965	2352
CCG CTT TCA GCC CCA AGT CCA ATC GGC AAG TGC GGG GAG CCG AAT CGA Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 1970 1975 1980	2400
TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 1985 1990 1995	2448
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 2000 2005	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 2015 2020 2025	2544
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2030 2035 2040 2045	2592
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2050 2055 2060	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2065 2070 2075	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2080 2085 2090	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2095 2100 2105	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2110 2115 2120 2125	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2130 2135 2140	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2145 2150 2155	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2160 2165 2170	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Asn Asn His Arg Ser Val Leu	3024

2175 2180 2185

	2113																
GTT Val 2190	Val	CCG Pro	GAA Glu	TGG Trp	GAA Glu 2195	Ala	GAA Glu	GTG Val	TCA Ser	CAA Gln 2200	GIU	GTT Val	CGT Arg	GTC Val	TGT Cys 2205	3072	
CCG Pro	GGT Gly	CGT Arg	GGC Gly	TAT Tyr 2210	Ile	CTT Leu	CGT Arg	GTC Val	ACA Thr 2215	GCG Ala	TAC Tyr	AAG Lys	GAG Glu	GGA Gly 2220	TAT	3120	
GGA Gly	GAA Glu	GGT Gly	TGC Cys 2225	Val	ACC Thr	ATT Ile	CAT His	GAG Glu 2230	Ile	GAG Glu	AAC Asn	AAT Asn	ACA Thr 2235	ASP	GAA Glu	3168	
CTG Leu	AAG Lys	TTT Phe 224	Ser	AAC Asn	TGT Cys	GTA Val	GAA Glu 224	GLu	GAA Glu	GTA Val	TAT Tyr	CCA Pro 2250	ASII	AAC Asn	ACG Thr	3216	
GTA Val	ACG Thr 225	Cys	AAT Asn	GAT Asp	TAT Tyr	ACT Thr 226	Ala	ACT Thr	CAA Gln	GAA Glu	GAA Glu 226	TYL	GAG Glu	GGT Gly	ACG Thr	3264	
TAC Tyr 227	Thr	TCT Ser	CGT Arg	AAT Asn	CGA Arg 227	Gly	TAT Tyr	GAC Asp	GGA Gly	GCC Ala 2280	Tyr	GAA Glu	AGC Ser	AAT Asn	TCT Ser 2285	3312	
TCT Ser	GTA Val	CCA Pro	GCT Ala	GAT Asp 229	Tyr	GCA Ala	TCA Ser	GCC Ala	TAT Tyr 229	GIU	GAA Glu	AAA Lys	GCA Ala	TAT Tyr 230	ACA Thr 0	3360	
GAT Asp	GGA Gly	CGA Arg	AGA Arg 230	Asp	AAT Asn	CCT	TGT Cys	GAA Glu 231	Ser	AAC Asn	AGA Arg	GGA Gly	TAT Tyr 231	GTA	GAT Asp	3408	
TAC Tyr	ACA Thr	CCA Pro 232	) Leu	CCA Pro	GCT Ala	GGC Gly	TAT Tyr 232	Val	ACA Thr	AAA Lys	GAA Glu	TTA Leu 233	GLU	TAC Tyr	TTC Phe	3456	,
CCA Pro	GAA Glu 233	Thi	GAT Asp	AAG Lys	GTA Val	TGG Trp 234	Ile	GAG Glu	ATC	GGA Gly	GAA Glu 234	Thr	GAA Glu	GGA Gly	ACA Thr	3504	t
TTC Phe 235	: Ile	GT(	G GAC L Asp	AGC Sei	GTG Val 235	. Glı	TTA Lev	CTI Lev	CTT Lev	ATG Met 236	GIU	GAA 1 Glu	TAA	∆G		3547	,

- (2) INFORMATION FOR SEQ ID NO:17:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1181 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15 Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 305 310 315

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala

340	345	350
340	3 1 3	

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Gln	Leu	Gly 355	Gln	Gly	Val	Tyr	Arg 360	Thr	Leu	Ser	Ser	Thr 365	Leu	Tyr	Arg
Arg	Pro 370	Phe	Asn	Ile	Gly	Ile 375	Asn	Asn	Gln	Gln	Leu 380	Ser	Val	Leu	Asp
Gly 385	Thr	Glu	Phe	Ala	Tyr 390	Gly	Thr	Ser	Ser	Asn 395	Leu	Pro	Ser	Ala	Val 400
Tyr	Arg	Lys	Ser	Gly 405	Thr	Val	Asp	Ser	Leu 410	Asp	Glu	Ile	Pro	Pro 415	Gln
Asn	Asn	Asn	Val 420	Pro	Pro	Arg	Gln	Gly 425	Phe	Ser	His	Arg	Leu 430	Ser	His
Val	Ser	Met 435	Phe	Arg	Ser	Gly	Phe 440	Ser	Asn	Ser	Ser	Val 445	Ser	Ile	Ile
Arg	Ala 450	Pro	Met	Phe	Ser	Trp 455	Ile	His	Arg	Ser	Ala 460	Glu	Phe	Asn	Asn
Ile 465	Ile	Pro	Ser	Ser	Gln 470	Ile	Thr	Gln	Ile	Pro 475	Leu	Thr	Lys	Ser	Thr 480
Asn	Leu	Gly	Ser	Gly 485	Thr	Ser	Val	Val	Lys 490	Gly	Pro	Gly	Phe	Thr 495	Gly
Gly	Asp	Ile	Leu 500		Arg	Thr	Ser	Pro 505	Gly	Gln	Ile	Ser	Thr 510	Leu	Arg
Val	Asn	Ile 515		Ala	Pro	Leu	Ser 520	Gln	Arg	Tyr	Arg	Val 525	Arg	Ile	Arg
Туr	Ala 530		Thr	Thr	Asn	Leu 535	Gln	Phe	His	Thr	Ser 540	Ile	Asp	Gly	Arg
Pro 545		Asn	Gln	Gly	Asn 550	Phe	Ser	Ala	Thr	Met 555	Ser	Ser	Gly	Ser	Asn 560
Leu	Gln	Ser	Gly	Ser 565		Arg	Thr	Val	Gly 570	Phe	Thr	Thr	Pro	Phe 575	Asn
Phe	Ser	Asn	Gly 580		Ser	Val	. Phe	Thr 585	Leu	Ser	Ala	His	Val 590	Phe	Asn
Ser	Gly	Asr 595		ı Val	. Tyr	· Ile	Asp 600	Arg	ılle	Glu	Phe	Val 605	Pro	Ala	Glu
Val	. Thr		e Glu	ı Ala	a Glu	Tyr 615	Asp	Leu	Glu	Arg	Ala 620	Gln	Lys	Ala	Val
Asr 625		ı Leı	ı Phe	e Thr	Ser 630	: Ser	Asn	Glr	ı Ile	635	Leu	Lys	Thr	Asp	Val 640
Thi	: Asy	у Туз	r His	5 Ile 645		Glr	ı Val	. Ser	650	ı Lev	ı Val	. Glu	ı Cys	655	Ser
Asp	Glu	ı Phe	e Cys		ı Asp	Glu	ı Lys	Lys 665	Glu	ı Let	ı Ser	Glu	Lys 670	: Val	Lys

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 770 780

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 850 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 865 870 875

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 900 905 910

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 945 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 980 985 990 Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 1000

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1015

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1040 1030

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1065

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1080

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1095

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1115 1110

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1130 1125

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1145 1140

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 1160 1155

Phe Ile Val Asp Ser Val Glu Leu Leu Met Glu Glu 1175 1170

- (2) INFORMATION FOR SEQ ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4817 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: join(1839..2141, 2239..2547, 2641..2718, 2794 ..2871, 3001..3135, 3236..3370)
  - (D) OTHER INFORMATION: /product= "maize TrpA" /note= "Maize TrpA sequence as disclosed in Figure 24."
    - (ix) FEATURE:

(A) NAME/KEY: TATA\_signal (B) LOCATION: 1594..1599

(ix) FEATURE:

(A) NAME/KEY: CAAT\_signal (B) LOCATION: 1495..1499

#### (ix) FEATURE:

(A) NAME/KEY: promoter (B) LOCATION: 39..1838

(D) OTHER INFORMATION: /function= "Promoter sequence used

in pCIB4433"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

, ,	~					
GAATTCGGAT (	CCATTAAAGA	AGTCTTTGAA	CAGATTCTAG	AGATCTAGTT	TAATGAGCTC	60
CCAAAAGTCT '	IGAAAAATT	CAGCGGGGAG	GCCATTAGGG	CAGGGGTACT	GTTATGTTTT	120
AAAGAGAACA	CCACTTTCTT	GATCTCTTCT	AAAGAGAAAT	GTTTTGTAAG	AAGGATCCTG	180
TCCTCCTCAT	CCAACCTTTT	CATCGGCAAA	TTTTTCATAG	AGATATTAGA	GGCAAGAGAG	240
GGGCCAAAAA	GATCCATGTA	AATGGAAGTG	GCCACCTGGT	TGATACCTCC	CTCATCTTCA	300
ACAGAAAATC	CATTATGAAA	AAGTGAATGG	ATTTTAAACT	CTTCTTTTTC	TTCCCTTTTG	360
CAATGAGCTG	AAAATATCTG	GTATTATTCT	CATCACCCTC	ATTAATGAAT	CTGTCCCTAG	420
CAATTTGCTT	TCTCTTGATC	CCTTCTGCAG	CCACCATGTT	TCTTAAATTC	CACTCCATAT	480
CAAGCTTTTC	CAATCTATCA	GAATCTGAGA	TGGCTGCAAT	CTCTCTCATT	TTCTCAAGGA	540
TATCGATGTT	ATCCATAAGG	TATTTCTTGA	ACTTCTTATA	TTTCCCTTCG	ACATTTATAT	600
TCCATCCTTT	CAACATTTTT	TTGTTCAATC	TTTTTTGTTT	TTTTCCTTTC	CAAACATCGA	660
TACATTTCCT	GCTCCTCACA	GGTAAGGACG	AGCTTTCAAA	AAACCTTCTG	CTTTAAAGTC	720
AGGTCTGAGC	CTCCAGCAAA	GCTCACATAT	CTAAAGTCCC	TCTTCTTAGT	TGGGACAGAG	780
TCAGTGCTAA	GACACATGGG	AACATGACCA	GAAAAAAAA	ATCATATTTA	GCCCAGAGAC	840
AACAATATTC	TTGTACTGCA	AGTCTCGTTA	TGGGCTAGCA	AAGGAATCTA	CCCAACTTCT	900
CAAATGTGTT	GGGATGTCAA	GTATATAGAC	TATTCATCAG	TTCCAACTCT	ATCAAACTGT	960
GCAGCTCAAT	TATAGAGTTG	AATAAAGTGC	TCCATCTATT	TGTTCTTATC	CTCATATTTG	1020
GTTAAGATAT	TAAAATCACC	TCCCACCAAC	ATTTAAAGTG	CACCATTTAA	AGTGGCTCGC	1080
GAGCACCAAA	CCGCTGAAAA	CCGGAAATGT	TTAGCACGTT	GGCAGCGGGA	CCCTTTTCTA	1140
TCTCATCGTG	TTCTTCGTTG	TCCACCACGG	CCCACGGGCC	AACGCTCCTC	CATCCTGTAG	1200
TGTAGAGTAT	ATTCCATTTG	CGACCGAGCC	GAGCATCGAT	CCAGCCACAC	TGGCCACTGC	1260
CAGCCAGCCA	TGTGGCACTC	CTACGTATAC	TACGTGAGGT	GAGATTCACT	CACATGGGAT	1320
GGGACCGAGA	TATTTTACTG	CTGTGGTTGT	GTGAGAGATA	ATAAAGCATT	TATGACGATT	1380
GCTGAACAGC	ACACACCATG	CGTCCAGATA	GAGAAAGCTT	TCTCTCTTTA	TTCGCATGCA	1440
TGTTTCATTA	TCTTTTATCA	TATATATATA	ACACATATTA	AATGATTCTT	CGTTCCAATT	1500

TATAATTCAT TTGACTTTTT TATCCACCGA TGCTCGTTTT ATTAAAAAAA ATATTATAAT	1560										
TATTGTTACT TTTTGTTGTA ATATTGTTTA GCATATAATA AACTTTGATA CTAGTATGTT	1620										
TCCGAGCAAA AAAAAATATT AATATTTAGA TTACGAGCCC ATTAATTAAT TATATTCGAG	1680										
ACAAGCGAAG CAAAGCAAAG CAAGCTAATG TTGCCCCTGC TGTGCATGCA GAGGCCCGCT	1740										
CTTGCTATAA ACGAGGCAGC TAGACGCGAC TCGACTCATC AGCCTCATCA ACCTCGACGA	1800										
AGGAGGAACG AACGGACAGG TTGTTGCACA GAAGCGAC ATG GCT TTC GCG CCC Met Ala Phe Ala Pro 1 5											
AAA ACG TCC TCC TCC TCC CTG CTG TCC TCG GCG TTG CAG GCA GCT CAG Lys Thr Ser Ser Ser Ser Leu Ser Ser Ala Leu Gln Ala Ala Gln 10 15 20	1901										
TCG CCG CCG CTG CTC CTG AGG CGG ATG TCG TCG ACC GCA ACA CCG AGA Ser Pro Pro Leu Leu Arg Arg Met Ser Ser Thr Ala Thr Pro Arg 25 30 35	1949										
CGG AGG TAC GAC GCG GCC GTC GTC ACT ACC ACC ACC ACT GCT AGA Arg Arg Tyr Asp Ala Ala Val Val Thr Thr Thr Thr Ala Arg 40 45 50	1997										
GCT GCG GCG GCT GCT GTC ACG GTT CCC GCC GCC CCG CCG CAG GCG GGC Ala Ala Ala Ala Val Thr Val Pro Ala Ala Pro Pro Gln Ala Gly 55	2045										
CGC CGC CGC CGG TGC CAC CAA AGC AAG CGG CGG CAC CCG CAG AGG AG	2093										
AGC CGT CCG GTG TCG GAC ACC ATG GCG GCG CTC ATG GCC AAG GGC AAG Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu Met Ala Lys Gly Lys 90 95 100	2141										
GTTCGTATAG TACGCGCGCG TGTCGTCGTC GTTATTTTGC GCATAGGCGC GGACATACAC	2201										
GTGCTTTAGC TAGCTAACAG CTAGATCATC GGTGCAG ACG GCG TTC ATC CCG TAC Thr Ala Phe Ile Pro Tyr 105	2256										
ATC ACC GCC GGC GAC CCG GAC CTA GCG ACG ACG GCC GAG GCG CTG CGT  Ile Thr Ala Gly Asp Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg  110 115 120	2304										
CTG CTG GAC GGC TGT GGC GCC GAC GTC ATC GAG CTG GGG GTA CCC TGC Leu Leu Asp Gly Cys Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys 125 130 135	2352										
TCG GAC CCC TAC ATC GAC GGG CCC ATC ATC CAG GCG TCG GTG GCG CGG Ser Asp Pro Tyr Ile Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg 140 145 150 155	2400										
GCT CTG GCC AGC GGC ACC ACC ATG GAC GCC GTG CTG GAG ATG CTG AGG Ala Leu Ala Ser Gly Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg 160 165 170	2448										

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GAG GTG ACG CCG GAG CTG TCG TGC CCC GTG GTG CTC CTC TCC TAC TAC Glu Val Thr Pro Glu Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr 175	2496
AAG CCC ATC ATG TCT CGC AGC TTG GCC GAG ATG AAA GAG GCG GGG GTC Lys Pro Ile Met Ser Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val 190 195 200	2544
CAC GGTAACTATA GCTAGCTCTT CCGATCCCCC TTCAATTAAT TAATTTATAG His	2597
TAGTCCATTC ATGTGATGAT TTTTGTTTTT CTTTTTACTG ACA GGT CTT ATA GTG Gly Leu Ile Val 205	2652
CCT GAT CTC CCG TAC GTG GCC GCG CAC TCG CTG TGG AGT GAA GCC AAG Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys 210 215 220	2700
AAC AAC CTG GAG CTG GTAGGTTGAA TTAAGTTGAT GCATGTGATG Asn Asn Asn Leu Glu Leu 225 230	2748
ATTTATGTAG CTAGATCGAG CTAGCTATAA TTAGGAGCAT ATCAG GTG CTG Val Leu Leu	2802
ACA ACA CCA GCC ATA CCA GAA GAC AGG ATG AAG GAG ATC ACC AAG GCT Thr Thr Pro Ala Ile Pro Glu Asp Arg Met Lys Glu Ile Thr Lys Ala 235 240 245	2850
TCA GAA GGC TTC GTC TAC CTG GTAGTTATAT GTATATATAG ATGGACGACG Ser Glu Gly Phe Val Tyr Leu 250 255	2901
TAACTCATTC CAGCCCCATG CATATATGGA GGCTTCAATT CTGCAGAGAC GACGAAGACC	2961
ACGACGACGA CTAACACTAG CTAGGGGCGT ACGTTGCAG GTG AGC GTG AAC GGA Val Ser Val Asn Gly 260	3015
GTG ACA GGT CCT CGC GCA AAC GTG AAC CCA CGA GTG GAG TCA CTC ATC Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg Val Glu Ser Leu Ile 265 270 275	3063
CAG GAG GTT AAG AAG GTG ACT AAC AAG CCC GTT GCT GTT GGC TTC GGC Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val Ala Val Gly Phe Gly 280 285	3111
ATA TCC AAG CCC GAG CAC GTG AAG CAGGTACGTA CGTAGCTGAC CAAAAAAAAC Ile Ser Lys Pro Glu His Val Lys 295 300	3165
TGTTAACAAG TTTTGTTTGA CAAGCCGGCT ACTAGCTAGC TAACAGTGAT CAGTGACACA	3225
CACACACACA CAG ATT GCG CAG TGG GGC GCT GAC GGG GTG ATC ATC GGC Gln Ile Ala Gln Trp Gly Ala Asp Gly Val Ile Ile Gly 305	3274
AGC GCC ATG GTG AGG CAG CTG GGC GAA GCG GCT TCT CCC AAG CAA GGC	3322

Ser Ala Met 315	Val Arg Glr 320	Leu Gly	Glu Ala Al	a Ser Pro Lys 5	Gln Gly 330	
CTG AGG AGG Leu Arg Arg	CTG GAG GAG Leu Glu Glu 335	TAT GCC Tyr Ala	AGG GGC AT Arg Gly Me 340	CG AAG AAC GCG et Lys Asn Ala	CTG CCA Leu Pro 345	3370
TGAGTCCATG A	ACAAAGTAAA	ACGTACAGA(	G ACACTTGA	TA ATATCTATCT	ATCATCTCGG	3430
AGAAGACGAC C	GACCAATAA A	AAATAAGCC	A AGTGGAAG	TG AAGCTTAGCT	GTATATACAC	3490
CGTACGTCGT C	CGTCGTCGTT (	CCGGATCGA'	r ctcggccg	GC TAGCTAGCAG	AACGTGTACG	3550
TAGTAGTATG T	TAATGCATGG	AGTGTGGAG	C TACTAGCT	AG CTGGCCGTTC	ATTCGATTAT	3610
AATTCTTCGC T	CTGCTGTGG '	ragcagatg	T ACCTAGTC	GA TCTTGTACGA	CGAAGAAGCT	3670
GGCTAGCTAG (	CCGTCTCGAT	CGTATATGT.	A CTGATTAA	TC TGCAGATTGA	АТАААААСТА	3730
CAGTACGCAT A	ATGATGCGTA	CGTACGTGT	G TATAGTTT	GT GCTCATATAT	GCTCCTCATC	3790
ACCTGCCTGA	TCTGCCCATC	GATCTCTCT	C GTACTCCT	TC CTGTTAAATG	CCTTCTTTGA	3850
CAGACACACC A	ACCACCAGCA	GCAGTGACG	C TCTGCACG	CC GCCGCTTTAA	GACATGTAAG	3910
ATATTTTAAG	AGGTATAAGA	TACCAAGGA	G CACAAATC	TG GAGCACTGGG	ATATTGCAAA	3970
GACAAAAAA	AAACAAAATT	AAAGTCCCA	C CAAAGTAG	AG ATAGTAAAGA	GGTGGATGGA	4030
TTAAAATTAT	CTCATGATTT	TTGGATCTG	C TCAAATAG	AT CGATATGGTA	TTCAGATCTA	4090
TGTTGTATAG	CCTTTTCATT	AGCTTTCTG	AAAAAAA	TG GTATGATGAG	TGCGGAGTAG	4150
CTAGGGCTGT	GAAGGAGTCG	GATGGGCTT	C CACGTACT	TG TTTGTGGCCC	TAGTCCGGTT	4210
CTATTTAGGT	CCGATCCGAG	TCCGGCATG	G TCCGGTTC	CA TACGGGCTAG	GACCAAGCTC	4270
GGCACGTGAG	TTTTAGGCCC	GTCGGCTAG	C CCGAGCAC	GA CCCGTTTTA	AACTGGCTAG	4330
GACTCGCCCA	TTTAATAAGA	CAAACATTO	C AAAAAAT	GC TCTATTTTT	ATTTAAAATA	4390
TATTGTTTAT	TTGTGAAATG	TGTATTAT	TT GTAATAT	TA TTATTGTATA	TAGTTATATC	4450
TTCAATTATG	АТТТАТАААТ	ATGTTTTT	TA TTATGAA	CTC AATTTTAAGT	TTGATTTATG	4510
CGTTGGCGGG	CTCGAGGAGG	CACGGTGAZ	AC ATTTTTG	GT CGGGCTTAAC	GGGTCGGCCC	4570
GGCCCGGTTC	GGCCCATCCA	CGGCCCAT	CC CGTGTCG	SCC TCGTTCGGTG	AGTTCAGCCC	4630
GTCGGACAAC	CCGTCCCCGG	CCCGGATA	AT TAATCGG	GCC TAACCGTGGC	GTGCTTAAAC	4690
GGTCCGTGCC	TCAACGGACC	GGGCCGCG	GG CGGCCCG	TTT GACATCTCTA	GTGGTGTGAT	4750
TAGAGATGGC	GATGGGAACC	GATCACTG.	AT TCCGTGT	GGA GAATTCGATA	TCAAGCTTAT	4810
CGATACC						4817

# (2) INFORMATION FOR SEQ ID NO:19:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
- Met Ala Phe Ala Pro Lys Thr Ser Ser Ser Ser Ser Leu Ser Ser Ala 1 5 10 15
- Leu Gln Ala Ala Gln Ser Pro Pro Leu Leu Arg Arg Met Ser Ser 20 25 30
- Thr Ala Thr Pro Arg Arg Arg Tyr Asp Ala Ala Val Val Thr Thr 35 40 45
- Thr Thr Thr Ala Arg Ala Ala Ala Ala Ala Val Thr Val Pro Ala Ala 50 55 60
- Pro Pro Gln Ala Gly Arg Arg Arg Cys His Gln Ser Lys Arg Arg 65 70 75 80
- His Pro Gln Arg Arg Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu 85 90 95
- Met Ala Lys Gly Lys Thr Ala Phe Ile Pro Tyr Ile Thr Ala Gly Asp 100 105 110
- Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg Leu Leu Asp Gly Cys 115 120 125
- Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys Ser Asp Pro Tyr Ile 130 135
- Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg Ala Leu Ala Ser Gly 145 150 155 160
- Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg Glu Val Thr Pro Glu 165 170 175
- Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr Lys Pro Ile Met Ser 180 185 190
- Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val His Gly Leu Ile Val 195 200 205
- Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys 210 220
- Asn Asn Asn Leu Glu Leu Val Leu Leu Thr Thr Pro Ala Ile Pro Glu 225 230 235 240
- Asp Arg Met Lys Glu Ile Thr Lys Ala Ser Glu Gly Phe Val Tyr Leu 245 250 255
- Val Ser Val Asn Gly Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg 260 265 270
- Val Glu Ser Leu Ile Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val 275 280 285

Ala V	/al ( 290	Gly I	Phe C	Sly I	[le	Ser 1 295	Lys	Pro	Glu	His	Val 300	Lys	GIn	me	Ala	
Gln 7	rp (	Gly A	Ala A	Asp (	Gly 310	Val :	Ile	Ile	Gly	Ser 315	Ala	Met	Val	Arg	Gln 320	
Leu (	Gly (	Glu i	Ala A	Ala : 325	Ser	Pro :	Lys	Gln	Gly 330	Leu	Arg	Arg	Leu	Glu 335	Glu	
Tyr 7	Ala		Gly 1 340	Met :	Lys	Asn	Ala	Leu 345	Pro							
(2)	INFO	RMAT	ION I	FOR	SEQ	ID N	0:20	):								
	(i)	(A (B (C	UENC: ) LE: ) TY: ) ST: ) TO	NGTH PE: RAND	: 13 nucl EDNE	49 b eic SS:	ase ació sino	pair 1	rs							
	(ii)	MOL	ECUL	E TY	PE:	cDNA	<b>L</b>									
(	iii)	HYP	OTHE	TICA	L: 1	10										
pc	oller	A) E) I-spe	TURE  A) NA  B) LO  O) OT  ecifi  in F	ME/K CATI HER .c ca	ON: INFO	31 DRMAT um de	TION	: /n dent	ote= pro	"cD tein	NA s kin	eque ase	nce	for as	maize	<b>)</b>
Q1	SCIO	sea	III F	rgur	.e						•					
	(xi)	SEÇ	QUENC	E DE	ESCR	IPTI	: NC	SEQ	ID N	0:20	:					
TG (	CAG A	ATC A	ATG C Met H	CAC ( His H	CAC (	CTC :	TCC Ser	Gly	CAG Gln 355	CCC Pro	AAC Asn	GTG Val	GTG Val	GGC Gly 360	CTC Leu	47
CGC Arg	GGC Gly	GCG Ala	TAC Tyr 365	GAG Glu	GAC Asp	AAG Lys	CAG Gln	AGC Ser 370	Val	CAC His	CTC Let	GTC 1 Val	ATO Met 375	GIL	G CTG 1 Leu	95
TGC Cys	GCG Ala	GGC Gly 380	GGG Gly	GAG Glu	CTC Leu	TTC Phe	GAC Asp 385	Arg	ATC	ATC	GCC Ala	C CG0 A Arg 390	1 GTZ	C CAC	TAC Tyr	143
ACG Thr	GAG Glu 395	Arg	GGC	GCC Ala	GCG	GAG Glu 400	Let	CTC Lev	CGC Arg	GC0 G Ala	2 ATC a Ile 40	e va.	G CAC	G ATO	C GTG e Val	191
CAC His 410	Thr	TGC Cys	CAC His	TCC Ser	ATG Met	Gly	GTC Val	ATO L Met	G CAC	C CGG S Arg	g As	C ATO	C AA( e Ly:	G CC	C GAG o Glu 425	
AAC Asn	TTC Phe	CTG Leu	CTG Leu	CTC Leu 430	Ser	AAG Lys	GA(	C GAC	G GA( 1 As) 43	o Al	G CC a Pr	G CT o Le	C AA u Ly	G GC s Al 44	C ACC a Thr 0	287
03.0				maa	· cmc	י ייייר	• <i>ጥጥ(</i>	~ <b>^</b>	CA	c cc	C GA	G CT	G CT	C AG	G GAC	335

Asp	Phe	Gly	Leu 445	Ser	· Va	.1 F	Phe	Phe	Lys 450	Glu	ı G	ly (	Glu	Leu	Le 45	u <i>I</i> 5	Arg	Asp	>		
ATC Ile	GTC Val	GGC Gly 460	AGC Ser	GCC Ala	TA Ty	C :	ſyr	ATC Ile 465	GCG Ala	CCC	C G o G	AG ( lu '	GTG Val	CTC Leu 470	,	.G I	AGG Arg	AA( Lys	3	38	3
TAC Tyr	GGC Gly 475	CCG Pro	GAG Glu	GC0 Ala	C GA	sp .	ATC Ile 480	TGG Trp	AGC Ser	GT(	C G l G	TÄ	GTC Val 485	ATG Met	CT Le	C' eu'	TAC Tyr	AT(	C . e	43	1
TTC Phe 490	CTC Leu	GCC Ala	GG(	GT(	1 P:	СТ ( со 95	CCC Pro	TTC Phe	TGG Trp	GC.	a G	AG Glu	AAC Asn	GAG Glu	AZ A	AC sn	GGC Gly	AT 11 50	-	47	79
	ACC Thr	GCC Ala	ATO	C CT E Le 51	u A	GA rg	GGG Gly	CAG Gln	CTT Leu	GA As	Ďτ	CTC Leu	TCC Ser	AGC Sei	G G	AG lu	CCA Pro 520	TG Tr	G p	52	27
CCA Pro	CAC His	ATC Ile	TC0 Se:	G CC	c c	GA ly	GCC Ala	AAG Lys	GAT Asp 530	n Le	C (	GTC Val	AAG Lys	AA(	<b>3</b> 11	TG et 35	CTC Leu	AA As	C n	51	75
ATC Ile	AAC Asr	CC0	AA Ly	~ ~	.G C	GG .rg	CTC Leu	ACG Thr 545	GCG Ala	TI Ph	ie (	CAG Gln	GTC Val	CTC Le		AT sn	CAC His	CC	A O	62	23
TGG Trp	ATC 116	: AA		A GA u As	sp G	GA ly	GAC Asp 560	Ala	G CCT	r GA	AC .	ACG Thr	CCG Pro	, ne	T G u A	AC .sp	AAC Asn	GT Va	T al	6	71
GTT Val 570	CTC		C AG p Ar	G C	eu I	AAG Lys 575	CAG	TT(	C AGO	G G(	CC la	ATG Met 580	V21	C CA n Gl	G T n F	TC he	AAG Lys		AA ys 35	7	19
		A TT a Le	G AG u Ar	g I	חר ז	א תריא.	GCT Ala	GG(	G TG Y Cy	S	TA eu 95	TCC Ser	GAZ Gli	A GA u Gl	.G G	SAG Slu	ATC Ile		CA nr	7	67
GG( Gl <sub>2</sub>	G CT y Le	u Lv	's G.	AG A	TG' et	Pne	Lys	S AS	C AT n Il 61	e A	sp	шу≎	, AS	T AA p As		AGC Ser		G A	CC hr	8	315
AT	T AC e Th		C G		7 C	ama	י אר א	\ CA	C GG s Gl	c T	ጥር	GCA	AA	S 11.	AC (	GGG Gly	CC(	C A	AG ys	8	363
CT Le	G TC u Se 63	A GA		GC G er G	AA lu	ATC Met	GA G1: 64	uг	A CT	'A A eu M	TG let	GAZ Glu	A GC 1 Al 64	a n	CT (	GAC Asr	GC'	T G a A	AC .sp	<u> </u>	911
Gl	C AA		GG T ly L	TA A eu ]	TT :le	GAC Asp	TA Ty	c cz	C GF	AA T Lu F	TC he	GT( Va:		C G	CA la	AC <i>I</i> Thi	A GT Va	_	AT lis	!	959
65 AT Me		AC A	AA C ys L	eu 1	SAT Asp 570	3.0		A GA u G	AG CZ Lu H:	rs i	CTT Leu 575	TA	C AC	CA G	CA la	TT( Phe	C CA e Gl 68		AT Yr	1	007
TI Pl	CC G	AC A sp L	AG G ys A			AG Se	C GG r Gl	G T	AC A' yr I	TT : le '	ACT Thr	' AA	A G	AA G lu G	AG lu	CT'	r GA u Gl	.G (	CAC His	1	055

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			685					690					695				
GCC T Ala I	Leu :	AAG Lys 700	GAG ( Glu (	CAA ( Gln (	GGG '	Leu '	TAT Tyr 705	GAC ( Asp .	GCC Ala	GAT Asp	AAA Lys	ATC Ile 710	AAA Lys	GAC Asp	ATC Ile	1103	
ATC T	TCC Ser 715	GAT Asp	GCC ( Ala	GAC (	Ser	GAC Asp 720	AAT Asn	GAT Asp	GGA Gly	AGG Arg	ATA Ile 725	GAT Asp	TAT Tyr	TCA Ser	GAG Glu	1151	
TTT ( Phe '	GTG Val	GCG Ala	ATG . Met	Met .	AGG Arg 735	Lys	GGG Gly	ACG Thr	GCT Ala	GGT Gly 740	GCC Ala	GAG Glu	CCA Pro	ATG Met	AAC Asn 745	1199	
ATC .	AAG Lys	AAG Lys	Arg	CGA Arg 750	GAC Asp	ATA Ile	GTC Val	CTA Leu	TAGT	(GAA	GTG P	AAGC?	AGCA	AG		1246	
TGTG	TAAT	rgt <i>i</i>	ATGI	GTAT	A GC	AGCI	CAA	A CAA	GCA	TTA	TGT	ACAT(	CTG '	TACA	CAAAT	G 1306	,
								A AAA								1349	,
(2)		(i) :	(A) (B) (D)	ENCE LEN TYI	CHAI IGTH: PE: 6	RACTI 408	ERIS' Bam cac	TICS ino a id ar	: acid	s							
			MOLE														
								: SE									
Gln 1	Ile	Met	His	His	Leu	Ser	Gly	Gln	Pro	Asn	Val	Val	Gly	. Leu	ı Arg		
				5					10					15	5		
			20	Asp				25	His	. Leu	ı Val	Met	Glu 30	Lev	ı Cys		
			20 Glu	Asp				25 Ile	His	. Leu	ı Val	Met	Glu 30	Lev			
Ala	Gly	Gly 35	20 Glu	Asp Leu	Phe	Asp	Arg 40	Zo Ille	His	Leu Ala	ı Val	Met Gly 45	Glu 30 Glr	Leu ) 1 Tyr	ı Cys	·	
Ala Glu	Gly Arg 50	Gly 35 Gly	20 Glu Ala	Asp Leu Ala	Phe Glu	Asp Leu 55	Arg 40	Ile Arg	His Ile	: Leu : Ala	Val Arg Val 60	Met Gly 45	Glu 30 Glr Glr	Lev Tyr	Cys		
Ala Glu Thr	Gly Arg 50	Gly 35 Gly His	20 Glu Ala Ser	Asp Leu Ala Met	Phe Glu Gly 70	Asp Leu 55 Val	Arg 40 Leu	Ile Arg	His Ile	Leu Ala Ila Asp 7:	Val Arg Val 60	Met Gly 45 Glr	Glu 30 Glr Glr i Ile	Leu Tyr Val	Thr His Asn 80 R Asp		
Ala Glu Thr 65	Gly Arg 50 Cys	Gly 35 Gly His	20 Glu Ala Ser	Asp Leu Ala Met	Glu Gly 70	Asp Leu 55 Val	Arg 40 Leu Met	Ile Arg His	His Ile Ala Arg	E Ala Ile Asp 7!	Val Arg 60 5 Ile	Met Gly Glr )	Glu 30 Glr Glr Glr Glr Glr Glr Glr Glr Glr Glr	Leu  Yal  O Glu  Thi  g Asj	Thr His Asn 80 R Asp		
Ala Glu Thr 65 Phe	Gly Arg 50 Cys Let	Gly 35 Gly His His Lev	20 Glu Ala Ser Leu Ser 100	Asp Leu Ala Met	Glu Gly 70 Lys	Asp Leu 55 Val	Arg 40 Lev Met	Ile Arg His Asp S Glu 105	His Ile Ala Arg	E Ala A Ile 7! Asp 7! Asp 7! Y Gl	Val Arg Val 60 D Ile	Met Gly 45 Glr ) Lys	Glu 30 Glr Glr Glr Are Are 11	Leu  Tyr  Val  Glu  Th:  9:  GRAS:	Thr His Asn 80 RASP		

Leu Ala Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe 145 150 150

Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro 165 170 175

His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile 180 185 190

Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp 195 200 205

Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val 210 215 220

Leu Asp Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala 225 230 235 240

Ala Leu Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly 245 250 255

Leu Lys Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile 260 265 270

Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu 275 280 285

Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly 290 295 300

Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met 305 310 315 320

Asn Lys Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe 325 330 335

Asp Lys Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala 340 345 350

Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile 355 360 365

Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe 370 375 380

Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile 385 390 395 400

Lys Lys Arg Arg Asp Ile Val Leu 405

- (2) INFORMATION FOR SEQ ID NO:22:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 464 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

#### (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: /note= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
  - Val Leu Gly Arg Pro Met Glu Asp Val Arg Ala Thr Tyr Ser Met Gly
  - Lys Glu Leu Gly Arg Gly Gln Phe Gly Val Thr His Leu Cys Thr His
  - Arg Thr Ser Gly Glu Lys Leu Ala Cys Lys Thr Ile Ala Lys Arg Lys
  - Leu Ala Ala Arg Glu Asp Val Asp Val Arg Arg Glu Val Gln Ile
  - Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala
  - Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly
  - Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg 105
  - Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val His Thr Cys 120
  - His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu Asn Phe Leu 135
  - Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr Asp Phe Gly 150
  - Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val Gly
  - Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro 185
  - Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala
  - Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala 215
  - Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro His Ile 225
  - Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile Asn Pro
  - Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp Ile Lys

260 265 270

Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val Leu Asp 275 280 285

Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala Ala Leu 290 295 300

Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly Leu Lys 305 310 315

Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile Thr Leu 325 330 335

Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu Ser Asp 340 345 350

Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly Asn Gly 355 360 365

Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met Asn Lys 370 380

Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe Asp Lys 385 390 395 400

Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala Leu Lys 405 410 415

Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile Ser Asp 420 425 430

Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe Val Ala 435 440 445

Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile Lys Lys 450 455 460

# (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 295 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..295
- (D) OTHER INFORMATION: /note= "rat protein kinase II protein sequence as shown in Figure 32."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val Lys Lys Thr Ser Thr Gln Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile His Gln Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Glu Gln Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu

Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His

235

Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met His Arg Gln 265

Glu Thr Val Glu Cys Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys 280

Gly Ala Ile Leu Thr Thr Met

# (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 142 amino acids

- (B) TYPE: amino acid(C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: Protein
    - (B) LOCATION: 1..142
- (D) OTHER INFORMATION: /note= "human calmodulin protein sequence as shown in Figure 33."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe 1 5 10 15

Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val

Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met 35 40

Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu 50 55 60

Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu 65 70 75 80

Glu Ile Arg Glu Ala Phe Arg Val Lys Asp Lys Asp Gly Asn Gly Tyr 85 90 95

Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys
100 105 110

Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Ile Asp 115 120 125

Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met 130 135 140

- (2) INFORMATION FOR SEQ ID NO:25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 463 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (ix) FEATURE:
    - (A) NAME/KEY: Protein
    - (B) LOCATION: 1..463

(D) OTHER INFORMATION: /note= \*protein sequence for soybean CDPK as shown in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Val Leu Pro Gln Arg Thr Gln Asn Ile Arg Glu Val Tyr Glu Val Gly
1 5 10 15

Arg Lys Leu Gly Gln Gly Gln Phe Gly Thr Thr Phe Glu Cys Thr Arg

Arg Ala Ser Gly Gly Lys Phe Ala Cys Lys Ser Ile Pro Lys Arg Lys 35 40 45

Leu Leu Cys Lys Glu Asp Tyr Glu Asp Val Trp Arg Glu Ile Gln Ile 50 55 60

Met His His Leu Ser Glu His Ala Asn Val Val Arg Ile Glu Gly Thr 65 70 75 80

Tyr Glu Asp Ser Thr Ala Val His Leu Val Met Glu Leu Cys Glu Gly . 85 90 95

Gly Glu Leu Phe Asp Arg Ile Val Gln Lys Gly His Tyr Ser Glu Arg 100 105 110

Gln Ala Ala Arg Leu Ile Lys Thr Ile Val Glu Val Val Glu Ala Cys 115 120 125

His Ser Leu Gly Val Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu 130 135 140

Phe Asp Thr Ile Asp Glu Asp Ala Lys Leu Lys Ala Thr Asp Phe Gly 145 150 155 160

Leu Ser Val Phe Tyr Lys Pro Gly Glu Ser Phe Cys Asp Val Val Gly 165 170 175

Ser Pro Tyr Tyr Val Ala Pro Glu Val Leu Arg Lys Leu Tyr Gly Pro 180 185 190

Glu Ser Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Ser 195 200 205

Gly Val Pro Pro Phe Trp Ala Glu Ser Glu Pro Gly Ile Phe Arg Gln 210 215 220

Ile Leu Leu Gly Lys Leu Asp Phe His Ser Glu Pro Trp Pro Ser Ile 225 230 235 240

Ser Asp Ser Ala Lys Asp Leu Ile Arg Lys Met Leu Asp Gln Asn Pro 245 250 255

Lys Thr Arg Leu Thr Ala His Glu Val Leu Arg His Pro Trp Ile Val 260 265 270

Asp Asp Asn Ile Ala Pro Asp Lys Pro Leu Asp Ser Ala Val Leu Ser 275 280 285

Arg Leu Lys Gln Phe Ser Ala Met Asn Lys Leu Lys Lys Met Ala Leu

290 295 300

Arg Val Ile Ala Glu Arg Leu Ser Glu Glu Glu Ile Gly Gly Leu Lys 305 310 315 320

Glu Leu Phe Lys Met Île Asp Thr Asp Asn Ser Gly Thr Ile Thr Phe 325 330 335

Asp Glu Leu Lys Asp Gly Leu Lys Arg Val Gly Ser Glu Leu Met Glu 340 345 350

Ser Glu Ile Lys Asp Leu Met Asp Ala Ala Asp Ile Asp Lys Ser Gly 355 360 365

Thr Ile Asp Tyr Gly Glu Phe Ile Ala Ala Thr Val His Leu Asn Lys 370 375 380

Leu Glu Arg Glu Glu Asn Leu Val Ser Ala Phe Ser Tyr Phe Asp Lys 385 390 395

Asp Gly Ser Gly Tyr Ile Thr Leu Asp Glu Ile Gln Gln Ala Cys Lys 405 410 415

Asp Phe Gly Leu Asp Asp Ile His Ile Asp Asp Met Ile Lys Glu Ile 420 425 430

Asp Gln Asp Asn Asp Gly Gln Ile Asp Tyr Gly Glu Phe Ala Ala Met 435 440 445

Met Arg Lys Gly Asn Gly Gly Ile Gly Arg Arg Thr Met Arg Lys 450 455 460

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4162 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1418..1427
  - (D) OTHER INFORMATION: /note= "start of mRNA"
- (ix) FEATURE:
  - (A) NAME/KEY: exon
  - (B) LOCATION: 1481..2366
- (ix) FEATURE:
  - (A) NAME/KEY: intron
  - (B) LOCATION: 2367..2451
- (ix) FEATURE:
  - (A) NAME/KEY: exon
  - (B) LOCATION: 2452..2602

(ix)	FEATU		
	(A)	NAME/KEY:	intron
	(B)	LOCATION:	26032690
(ix)	FEATU	JRE:	
•	(A)	NAME/KEY:	exon
		LOCATION:	
	(-,		
(ix)	FEATU	JRE:	
( === /	(A)	NAME/KEY:	intron
	(B)	LOCATION:	28052906
	(1)	HOCHIT TOTAL	
(iv)	FEATU	TRE	
(17)		NAME/KEY:	exon
	(A)	TOCATION:	29073075
	(5)	DOCATION.	250,,,,,,
(122)	FEAT	mpr.	
(17)	(7)	NAME/KEY:	intron
	(E)	TOCATION:	30763177
	(D)	LOCATION.	30,0
/ix\	FEAT	ישם.	
(IX)	LEWI.	NAME/KEY:	exon
	(27)	TOCATTON.	31783304
	(B)	LOCATION.	31703301
/:\	FEAT	mr.	
(IX)	LEAT	NAME/KEY:	intron
	(A)	NAME/ REI:	33053398
	(B)	LOCATION:	33033330
4		TIDE!	
(ix)			01107
	(A)	NAME/KEY:	2200 2409
	(B)	LOCATION:	33993498
,		· · · ·	
(ix)		UKE:	intron
	(A)	NAME/KEY:	34993713
	(B)	LOCATION:	34993/13
(ix)	FEAT		
	/ h \	NIAME/KEV	exon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(B) LOCATION: 3714..3811

TTAGTAACAC CTCTCCAATC GCTTGGGTTG GCACATTCTT AGCTTTTATC ACATTTTAAG 60 AAATAGAGTT CACCACCTTC AAAATAATGC CTATACAATG AATGATCGCT TGGATGCAAT 120 ATAGCTAGAT TCAACTAGCT ATATATGGTC AATAGAACCC TGTGAGCACC TCACAAACAC 180 GACTTCAATT TTGAGACCCT AAGCGAGTAA ATGGTTAAAG TCCTCTTATT ATTAGTCTTA 240 GGACTTCTCC TTGCTAAATG CTTGTCAGCG ATCTATATAT CTTCCCCACT GCGGGAGATA 300 CTATATATAG GGCCTTGGAC CTCTAGGGTA TCTCAAAGGC CTAGTCACAA CAATTCTCAA 360 CAGTATTTAA TTTTATACAT GTATGAACAG TGTAGGAATT TGAGTGCCCA ACCCAAGAGT 420 GGGAGGTGTA AATTGGGTAG CTAAACTTAA ATAGGGCTCT TCTTATTTAG GTTTATCTAG 480 TCTCTACTTA GACTAATTCA GAAAGAATTT TACAACCTAT GGTTAATCAT ATCTCTAGTC 540 TAAGCAAATT TAGGAAAGTT AAAAGCACAC AATTAGGCAC ATGTGAAAGA TGTGTATGGT 600 AAGTAAAAGA CTTATAAGGA AAAAGTGGGT GAATCCTCAA GATGTGGTGG TATATCCCAA 660 TGATATTAGA TGCCAGAATA TAGGGGGGAA ATCGATGTAT ACCATCTCTA CCAGGATACC 720 TGTGCGGACT GTGCAACTGA CACATGGACC ATGGTGTCTT CTTAGATTTG GTTATTAGCT 780 AATTGCGCTA CAACTTGTTC AAGGCTAGAC CAAATTAAAA AACTAATATT AAACATAAAA 840 AGTTAGGCAA ACTATAGTAA ATTATGCAGC GATCCAACAA CAAGCCATGT CTCGTGGGTC 900 ATGAGCCACG CGTCGGCCAT ACACCCACAT GATGTTTCCA TACGGATGGT CCTTATGCAA 960 TTTTGTCTGC AAAACACAAG CCTTAATACA GCCACGCGAC AATCATGGAA GTGGTCGTTT 1020 TAGGTCCTCA TCATGAAGTT CAGGGAAAAC GCATCAAATG TAATGCAGAG AAATGGTATT 1080 TCTTCTCTTG TAAATCAGGG AGAGGAGTAC CATCAGTACA GATTCAGAAT CAGAATTCAG 1140 TCTTCCAACG ACAATAATCG CAGCATCTTG TAAAAATTTG CAGAAACTTC TGTTTGACTT 1200 GTAGCCCTGA CCTTTGCAAA TATTTGAAGT TGTGCCTGCT GACACAACTT CAATCTGGAA 1260 GTGCTGTTGA TCAGTTTTGC CAGAAACAGC AAGCAGCCTA TATATATCTG TCACGAGACA 1320 CCCTGCCGCC CTCTTCTTTC CCGCCATTCC CTCCCTACCC TTCAAAATCT AGAAACCTTT 1380 TTTTTTCCTC CCGATACGCC CCTCCATCTC TCGCCGTTCA TGTCCGTGGC TGGCTGCCCT 1440 CCGTGGGAGC AGGCGGCCGC ACTCGTTCCC CGCCGCAGCC ATGGGCCAGT GCTGCTCCAA 1500 GGGCGCCGGA GAGGCCCCGC CACCGAGGCG CCAAACGGCA GGCGCCAAGC CGCGGGCGTC 1560 CGCGAACAAC GCCGACGGAC AACGGGCGTC GTCCTCGTCC GCGGTGGCTG CTGCCGCTGC 1620 TGCTGCCGGT GGTGGTGGCG GCGGCACGAC GAAGCCGGCC TCACCCACCG GCGGCGCCAG 1680 GGCCAGCTCC GGCAGCAAAC CGGCGGCGGC CGTGGGCACG GTGCTGGGCC GGCCCATGGA 1740 GGACGTGCGC GCGACCTACT CGATGGGCAA GGAGCTCGGG CGCGGGCAGT TCGGCGTGAC 1800 GCACCTGTGC ACGCACCGGA CGAGCGGCGA GAAGCTGGCG TGCAAGACGA TCGCGAAGCG 1860 GAAGCTGGCG GCCAGGGAGG ACGTGGACGA CGTGCGGCGG GAGGTGCAGA TCATGCACCA 1920 CCTCTCCGGC CAGCCCAACG TGGTGGGCCT CCGCGGCGCG TACGAGGACA AGCAGAGCGT 1980 GCACCTCGTC ATGGAGCTGT GCGCGGGCGG GGAGCTCTTC GACCGCATCA TCGCCCGGGG 2040 CCAGTACACG GAGCGCGGCG CCGCGGAGCT GCTGCGCGCC ATCGTGCAGA TCGTGCACAC 2100 CTGCCACTCC ATGGGGGTGA TGCACCGGGA CATCAAGCCC GAGAACTTCC TGCTGCTCAG 2160 CAAGGACGAG GACGCGCCGC TCAAGGCCAC CGACTTCGGC CTCTCCGTCT TCTTCAAGGA 2220 GGGCGAGCTG CTCAGGGACA TCGTCGGCAG CGCCTACTAC ATCGCGCCCG AGGTGCTCAA 2280 GAGGAAGTAC GGCCCGGAGG CCGACATCTG GAGCGTCGGC GTCATGCTCT ACATCTTCCT 2340

CGCCGGCGTG (	ССТСССТТСТ	GGGCAGGTCG	GATCCGTCCG	TGTTCGTCCT	AGACGATATA	2400
CAGAACCCGA (	CGATGGATTT	GCTTCTCAGC	CCTGTTCTTG	CATCACCAGA	GAACGAGAAC	2460
GGCATCTTCA	CCGCCATCCT	GCGAGGGCAG	CTTGACCTCT	CCAGCGAGCC	ATGGCCACAC	2520
ATCTCGCCGG	GAGCCAAGGA	TCTCGTCAAG	AAGATGCTCA	ACATCAACCC	CAAGGAGCGG	2580
CTCACGGCGT	TCCAGGTCCT	CAGTAAGTAC	CCAGATCGTT	GCTGTCATAC	ACTCATATGA	2640
ATTGTATCGT	TCATGAGCAA	CGATCGAGCG	GATTTGGTGA	ACTTGTAGAT	CACCCATGGA	2700
TCAAAGAAGA	CGGAGACGCG	CCTGACACGC	CGCTTGACAA	CGTTGTTCTC	GACAGGCTCA	2760
AGCAGTTCAG	GGCCATGAAC	CAGTTCAAGA	AAGCAGCATT	GAGGGTACAT	TATCTGATAA	2820
AAGCTCCACA	AATACAACTT	CTGAAGAACA	GCAATGCTTA	CACGGCAGAA	TTTTCATTAT	2880
AAATGCTCTT	GATGACATAA	TGTTAGATCA	TAGCTGGGTG	CCTATCCGAA	GAGGAGATCA	2940
CAGGGCTGAA	GGAGATGTTC	AAGAACATTG	ACAAGGATAA	CAGCGGGACC	ATTACCCTCG	3000
ACGAGCTCAA	ACACGGGTTG	GCAAAGCACG	GGCCCAAGCT	GTCAGACAGC	GAAATGGAGA	3060
AACTAATGGA	AGCAGTGAGT	TTTCAGAGTA	СААТСТТААА	AAAAGGAATT	GTGATTCTTT	3120
TCAAAATGAA	GAAGTAATCT	GAAAACATCC	CTGCTGAAAT	GCTTTATACA	TTTCCAGGCT	3180
GACGCTGACG	GCAACGGGTT	AATTGACTAC	GACGAATTCG	TCACCGCAAC	AGTGCATATG	3240
AACAAACTGG	ATAGAGAAGA	GCACCTTTAC	ACAGCATTCC	AGTATTTCGA	CAAGGACAAC	3300
AGCGGGTAAG	TTGAACGTTA	AAATGATACA	GCTGGTACCT	GAATTCTGGA	CAACACATAT	3360
CATAACAGGA	CACATATATA	ATTCGTTTAT	CTCACAGGTA	CATTACTAA	GAAGAGCTTG	3420
AGCACGCCTT	GAAGGAGCAA	GGGTTGTATG	ACGCCGATAA	AATCAAAGAC	ATCATCTCCG	3480
ATGCCGACTC	TGACAATGTA	AGGAACAAAC	: ATTATTTAAA	TTTCAGCCG	CAAACTAAAC	3540
TATAGAAACC	ACATCATGAT	ATCAAATTTI	GAGGTGGCGG	TGCTACAGA	A ATAGAACCCA	3600
GTACACCAAA	ATGACTAACT	TGTCATGAT	AGTTGTTCCT	CGTAACTGA	A CATTTGTGTT	3660
CTTAGTTTCT	TATTGTTAA	A CCAAAGACTT	T AAATTCACT	TTGCACATG	AGGATGGAAG	3720
GATAGATTAT	TCAGAGTTT	G TGGCGATGA	r gaggaaagg	ACGGCTGGT	G CCGAGCCAAT	3780
GAACATCAAG	: AAGAGGCGA	G ACATAGTCC	r atagtgaagi	r gaagcagaa	G TGTGTAATGT	3840
AATGTGTATA	GCAGCTCAA	A CAAGCAAAT	r TGTACATCT	G TACACAAAT	G CAATGGGGTT	3900
ACTTTTGCA	CTTAGTTCA	r ggatggttg	r GTACGTTGT	G CTATTGATT	G CAAGTGATTT	3960
GAAAGACATO	CATACTTAG	G AACTGAGAA	A GATAGATCT	A CTACTGCTA	G AGACAGAACA	4020
ATAGGATAA	r TCAGAAGTG	G TATTTCAGA	A GACTACAGC	T GGCATCTAT	T ATTCTCATTG	4080
					A TCGAGCTCCC	4140
	r CGTATTAGG					4162

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3546 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO

540

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid maize optimized heat stable cryIA(b)" /note= "DNA sequence as disclosed in Figure 37 as contained in pCIB5515."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG Met	GAC Asp 410	AAC Asn	AAC Asn	CCC Pro	AAC Asn	ATC Ile 415	AAC Asn	GAG Glu	TGC Cys	ATC Ile	CCC Pro 420	TAC Tyr	AAC Asn	TGC Cys	CTG Leu		48
AGC Ser 425	AAC Asn	CCC Pro	GAG Glu	GTG Val	GAG Glu 430	GTG Val	CTG Leu	GGC Gly	GGC Gly	GAG Glu 435	CGC Arg	ATC Ile	GAG Glu	ACC Thr	GGC Gly 440		96
TAC Tyr	ACC Thr	CCC Pro	ATC Ile	GAC Asp 445	ATC Ile	AGC Ser	CTG Leu	AGC Ser	CTG Leu 450	ACC Thr	CAG Gln	TTC Phe	CTG Leu	CTG Leu 455	AGC Ser	1	44
GAG Glu	TTC Phe	GTG Val	CCC Pro 460	GGC Gly	GCC Ala	GGC Gly	TTC Phe	GTG Val 465	CTG Leu	GGC Gly	CTG Leu	GTG Val	GAC Asp 470	ATC Ile	ATC Ile	1	92
TGG Trp	GGC Gly	ATC Ile 475	TTC Phe	GGC Gly	CCC Pro	AGC Ser	CAG Gln 480	TGG Trp	GAC Asp	GCC Ala	TTC Phe	CTG Leu 485	GTG Val	CAG Gln	ATC Ile	2	40
GAG Glu	CAG Gln 490	Leu	ATC Ile	AAC Asn	CAG Gln	CGC Arg 495	ATC Ile	GAG Glu	GAG Glu	TTC Phe	GCC Ala 500	CGC Arg	AAC Asn	CAG Gln	GCC Ala	2	88
ATC Ile 505	Ser	CGC Arg	CTG Leu	GAG Glu	GGC Gly 510	CTG Leu	AGC Ser	AAC Asn	CTG Leu	TAC Tyr 515	Gln	ATC Ile	TAC Tyr	GCC Ala	GAG Glu 520	3	336
AGC Ser	TTC Phe	CGC Arg	GAG Glu	TGG Trp 525	Glu	GCC Ala	GAC Asp	CCC Pro	ACC Thr 530	Asn	CCC Pro	GCC Ala	CTG Leu	CGC Arg 535	GAG Glu	3	884
GAG Glu	Met	Arg	ATC	Gln	Phe	Asn	Asp	Met	AAC Asn	Ser	Ala	Leu	ACC Thr	Thr	GCC Ala	4	132

545

ATC Ile	CCC Pro	CTG Leu 555	TTC Phe	GCC Ala	GTG Val	CAG Gln	AAC Asn 560	TAC Tyr	CAG Gln	GTG Val	CCC Pro	CTG Leu 565	CTG Leu	AGC Ser	GTG Val	480
TAC Tyr	GTG Val 570	CAG Gln	GCC Ala	GCC Ala	AAC Asn	CTG Leu 575	CAC His	CTG Leu	AGC Ser	GTG Val	CTG Leu 580	CGC Arg	GAC Asp	GTC Val	AGC Ser	528
GTG Val 585	TTC Phe	GGC Gly	CAG Gln	CGC Arg	TGG Trp 590	GGC Gly	TTC Phe	GAC Asp	GCC Ala	GCC Ala 595	ACC Thr	ATC Ile	AAC Asn	AGC Ser	CGC Arg 600	576
TAC Tyr	AAC Asn	GAC Asp	CTG Leu	ACC Thr 605	CGC Arg	CTG Leu	ATC Ile	GGC Gly	AAC Asn 610	TAC Tyr	ACC Thr	GAC Asp	CAC His	GCC Ala 615	GTG Val	624
CGC Arg	TGG Trp	TAC Tyr	AAC Asn 620	ACC Thr	GGC Gly	CTG Leu	GAG Glu	CGC Arg 625	GTG Val	TGG Trp	GGT Gly	CCC Pro	GAC Asp 630	AGC Ser	CGC Arg	672
GAC Asp	TGG Trp	ATC Ile 635	AGG Arg	TAC Tyr	AAC Asn	CAG Gln	TTC Phe 640	CGC Arg	CGC Arg	GAG Glu	CTG Leu	ACC Thr 645	CTG Leu	ACC Thr	GTG Val	720
CTG Leu	GAC Asp 650	ATC Ile	GTG Val	AGC Ser	CTG Leu	TTC Phe 655	CCC Pro	AAC Asn	TAC Tyr	GAC Asp	AGC Ser 660	Arg	ACC Thr	TAC Tyr	CCC Pro	768
ATC Ile 665	CGC Arg	ACC Thr	GTG Val	AGC Ser	CAG Gln 670	CTG Leu	ACC Thr	CGC Arg	GAG Glu	ATT Ile 675	TAC Tyr	ACC Thr	AAC Asn	CCC Pro	GTG Val 680	816
CTG Leu	GAG Glu	AAC Asn	TTC Phe	GAC Asp 685	GGC Gly	AGC Ser	TTC Phe	CGC Arg	GGC Gly 690	Ser	GCC Ala	CAG Gln	GGC Gly	ATC Ile 695	GAG Glu	864
GGC Gly	AGC Ser	ATC Ile	CGC Arg 700	Ser	CCC Pro	CAC His	CTG Leu	ATG Met 705	Asp	ATC Ile	CTG	AAC Asn	AGC Ser 710	ATC Ile	ACC Thr	912
ATC Ile	TAC Tyr	ACC Thr 715	Asp	GCC Ala	CAC His	CGC Arg	GGC Gly 720	Glu	TAC Tyr	TAC Tyr	TGG	AGC Ser 725	GTA	CAC His	CAG Gln	960
ATC Ile	ATG Met 730	. Ala	AGC Ser	CCC Pro	GTC Val	GGC Gly 735	Phe	AGC Ser	GGC Gly	CCC Pro	GAG Glu 740	Pne	ACC Thr	TTC Phe	CCC	1008
CTG Leu 745	Tyr	GGC Gly	ACC Thr	ATG Met	GGC Gly 750	Asr	GCT Ala	GCA Ala	CCT Pro	CAG Gln 755	GII	GCC Arg	: ATC	GTG Val	GCA Ala 760	1056
CAG Gln	CTO Lev	GGC Gly	CAG Gln	GGA Gly 765	v Val	TAC Tyr	CGC Arg	ACC Thi	CTG Leu 770	ı Ser	: AGC	ACC Thr	CTG	TAC Tyr 775	CGT Arg	1104
CGA Arg	CCT Pro	TT(	AAC Asr 780	ı Ile	GGC Gly	ATO	C AAC e Asr	AAC A Asi 785	ı Gir	G CAG	CT(	G AGC	790	. Let	GAC Asp	1152

GGC Gly	ACC Thr	GAG Glu 795	TTC Phe	GCC Ala	TAC Tyr	GGC Gly	ACC Thr 800	AGC Ser	AGC Ser	AAC Asn	CTG Leu	CCC Pro 805	AGC Ser	GCC Ala	GTG Val	1200
TAC Tyr	CGC Arg 810	AAG Lys	AGC Ser	GGC Gly	ACC Thr	GTG Val 815	GAC Asp	AGC Ser	CTG Leu	GAC Asp	GAG Glu 820	ATC Ile	CCC Pro	CCT Pro	CAG Gln	1248
AAC Asn 825	AAC Asn	AAC Asn	GTG Val	CCA Pro	CCT Pro 830	CGA Arg	CAG Gln	GGC Gly	TTC Phe	AGC Ser 835	CAC His	CGT Arg	CTG Leu	AGC Ser	CAC His 840	1296
GTG Val	AGC Ser	ATG Met	TTC Phe	CGC Arg 845	AGT Ser	GGC Gly	TTC Phe	AGC Ser	AAC Asn 850	AGC Ser	AGC Ser	GTG Val	AGC Ser	ATC Ile 855	ATC Ile	1344
Arg	Ala	Pro	Met 860	Phe	Ser	Trp	Ile	His 865	CGC Arg	Ser	Ala	GIU	870	ASII	ASII	1392
Ile	Ile	Pro 875	Ser -	Ser	Gln	Ile	Thr 880	Gln	ATC Ile	Pro	Leu	885	ьys	ser	1111	1440
Asn	Leu 890	Gly	Ser	Gly	Thr	Ser 895	Val	Val	AAG Lys	Gly	900	GTĀ.	Pne	THE	GIY	1488
Gly 905	Asp	Ile	Leu	Arg	Arg 910	Thr	Ser	Pro	GGC Gly	915	lle	ser	THE	ьеи	920	1536
Val	Asn	Ile	Thr	Ala 925	Pro	Leu	Ser	Gln	CGC Arg 930	Tyr	Arg	vai	Arg	935	Arg	1584
Tyr	Ala	Ser	Thr 940	Thr	Asn	Leu	Gln	945		Thr	Ser	TIE	950	GTĀ	Arg	1632
Pro	Ile	Asn 955	Gln	Gly	Asn	Phe	Ser 960	Ala		Met	Ser	965	GIY	Ser	ASII	1680
Leu	Gln 970	Ser	Gly	Ser	Phe	Arg 975	Thr	· Val	. Gly	Phe	980	Thr	Pro	Pne	AAC Asn	1728
Phe 985	Ser	Asn	Gly	Ser	990	Val	Phe	Thr	Leu	995	Ala	. His	vaı	Pne	AAC Asn 1000	1776
Ser	Gly	Asr.	ı Glu	100	. Tyr )5	: Ile	: Asr	Arç	Ile 101	.0	ı Pne	e vai	. Pro	101		1824
GT0 Val	ACC Thr	TTC Phe	GAG Glu 102	ı Ala	GAG Glu	TAC Tyr	GAC Asr	CTC Lev 102	ı Glu	AGG Arg	GCT Ala	CAG Glr	AAG Lys 103	Ala	GTG Val	1872
AAC	GAG	G CTC	G TTC	: ACC	AGC	AGC	: AAC	CAC	ATC	GGC	C CTC	AAC	ACC	GAC	GTG	1920

Asn Glu Leu 1035		Ser Ser	Asn Gln 1040	Ile(	Gly Leu	Lys Thr 1045	Asp	Val	
ACC GAC TAC Thr Asp Tyr 1050	CAC ATC His Ile	GAT CAA Asp Gln 1059	Val Ser	AAT '	TTA GTT Leu Val 106	GIU CYS	TTA Leu	TCT Ser	1968
GAT GAA TTT Asp Glu Phe 1065	TGT CTG Cys Leu	GAT GAA Asp Glu 1070	AAA AAA Lys Lys	GIU.	TTG TCC Leu Ser 1075	GAG AAA Glu Lys	GTC Val	AAA Lys 1080	2016
CAT GCG AAG His Ala Lys	CGA CTT Arg Leu 108	_Ser Asp	GAG CGG Glu Arg	AAT Asn 1090	Leu Leu	CAA GAT Gln Asp	CCA Pro 1095	Non.	2064
TTT AGA GGG Phe Arg Gly	ATC AAT Ile Asn 1100	AGA CAA Arg Gln	CTA GAC Leu Asp 110	Arg	GGC TGG Gly Trp	AGA GGA Arg Gly 111	Ser	ACG Thr	2112
GAT ATT ACC Asp Ile Thr 1115	Ile Gln	GGA GGC Gly Gly	GAT GAC Asp Asp 1120	GTA Val	TTC AAF	A GAG AAT Glu Asn 1125	TAC Tyr	GTT Val	2160
ACG CTA TTG Thr Leu Leu 1130	GGT ACC	TTT GAT Phe Asp 113	_Glu Cys	TAT	CCA ACC Pro Thi	r Tyr Leu	TAT Tyr	CAA Gln	2208
AAA ATA GAT Lys Ile Asp 1145	GAG TCG Glu Ser	AAA TTA Lys Leu 1150	AAA GCC	TAT Tyr	ACC CG Thr Arg 1155	r TAC CAA g Tyr Gln	TTA Leu	AGA Arg 1160	2256
GGG TAT ATC Gly Tyr Ile	GAA GAT Glu Asp 116	Ser Glr	GAC TTA Asp Lev	GAA Glu 1170	IIe TY	r TTA ATT r Leu Ile	CGC Arg 117	TAT	2304
AAT GCC AAA Asn Ala Lys	CAC GAA His Glu 1180	A ACA GTA 1 Thr Val	AAT GTO Asn Val	Pro	GGT ACC	G GGT TCC r Gly Ser 119	neu	TGG Trp	2352
CCG CTT TCA Pro Leu Ser 119	GCC CCA Ala Pro	Ser Pro	ATC GGA Tle Gly 1200	A AAA Y Lys	TGT GG Cys Gl	G GAG CCC y Glu Pro 1205	AAT Asn	CGA Arg	2400
TGC GCT CCG Cys Ala Pro 1210	CAC CTO	G GAG TGO 1 Glu Try 12:	Asn Pro	G GAC o Asp	Leu As	C TGC AGO p Cys Sei 20	TGC Cys	AGG Arg	2448
GAC GGG GAG Asp Gly Glu 1225	AAG TGG	C GCC CAT s Ala Hi: 1230	CAT TC	C CAT r His	CAT TT His Ph 1235	C TCC TT( e Ser Le	G GAC 1 Asp	ATT Ile 1240	2496
GAT GTT GGA Asp Val Gly	TGT AC	r Asp Le	A AAT GA 1 Asn Gl	G GAC u Asp 125	ren er	T GTA TGO y Val Tr	G GTG o Val 125		2544
TTC AAG ATT Phe Lys Ile	T AAG AC Lys Th 1260	G CAA GA r Gln As	r GGC CA p Gly Hi 12	s Ala	AGA CT Arg Le	A GGA AA u Gly As: 12	n neo	A GAA 1 Glu	2592
TTT CTC GAA	A GAG AA ı Glu Ly	A CCA TT s Pro Le	A GTA GG u Val Gl	A GAA y Glu	GCA CT	TA GCT CG eu Ala Ar	T GTO g Val	AAA Lys	2640

1275 1280 1285

		213														
AGA G Arg A 1	CG G la G .290	AG A	AAA i	AAA Lys	Trp .	AGA Arg 1295	Asp	AAA Lys	CGT Arg	GIU	AAA Lys 1300	Leu	GAA Glu	TGG Trp	GAA Glu	2688
ACA A Thr A 1305	AT A	TT (	GTT '	Tyr	AAA Lys 1310	Glu	GCA Ala	AAA Lys	GAA Glu	TCT Ser 1315	vaı	GAT Asp	GCT Ala	TTA Leu	TTT Phe 1320	2736
GTA A	AAC T Asn S	CT (	Gln	TAT Tyr 1325	Asp	AGA Arg	TTA Leu	CAA Gln	GCG Ala 1330	Asp	ACC Thr	AAC Asn	ATC Ile	GCG Ala 1335	Mec	2784
ATT (	CAT G	la .	GCA Ala 1340	Asp	AAA Lys	CGC Arg	GTT Val	CAT His 1345	Ser	ATT Ile	CGA Arg	GAA Glu	GCT Ala 1350	TĀT	CTG Leu	2832
CCT (	Glu I	TG eu .355	Ser	GTG Val	ATT Ile	CCG Pro	GGT Gly 136	Val	AAT Asn	GCG Ala	GCT Ala	ATT Ile 1365	Pne	GAA Glu	GAA Glu	2880
TTA (	GAA G Glu G 1370	GG Sly	CGT Arg	ATT Ile	TTC Phe	ACT Thr 1375	Ala	TTC Phe	TCC Ser	CTA Leu	TAT Tyr 1380	ASP	GCG Ala	AGA Arg	AAT Asn	2928
GTC 7 Val 1 1385	Ile I	AAA Lys	AAT Asn	GGT Gly	GAT Asp 139	Phe	AAT Asn	AAT Asn	GGC Gly	TTA Leu 139	Ser	TGC Cys	TGG Trp	AAC Asn	GTG Val 1400	2976
AAA (	GGG ( Gly I	CAT	GTA Val	GAT Asp 140	Val	GAA Glu	GAA Glu	CAA Gln	AAC Asn 141	Asn	CAC His	CGT Arg	TCG Ser	GTC Val 141	ьеα	3024
GTT Val	GTT ( Val 1	CCG Pro	GAA Glu 142	Trp	GAA Glu	GCA Ala	GAA Glu	GTG Val 142	Ser	CAA Gln	GAA Glu	GTT Val	CGT Arg 143	var	TGT Cys	3072
CCG Pro	Gly A	CGT Arg 1439	Gly	TAT Tyr	ATC Ile	CTT Leu	CGT Arg 144	Val	ACA Thr	GCG Ala	TAC Tyr	AAG Lys 144	GIU	GGA Gly	TAT Tyr	3120
GGA Gly	GAA Glu 1450	Gly	TGC Cys	GTA Val	ACC Thr	ATT Ile 145	His	GAG Glu	ATC	GAG Glu	AAC Asn 146	Asn	ACA Thr	GAC Asp	GAA Glu	3168
CTG Leu 1465	Lys	TTT Phe	AGC Ser	AAC Asn	TGT Cys 147	Val	GAA Glu	GAC	GAA Glu	GTA Val	. Tyr	CCA Pro	AAC Asn	: AAC Asr	ACG Thr 1480	3216
GTA Val	ACG Thr	TGT Cys	AAT Asn	GAT Asp 148	Туг	ACT Thr	GCC Ala	ACT Thr	CAA Glr 149	GII	A GAA 1 Glu	TAT 1 Tyr	GAC Glu	G GGT 1 Gly 149	ACG Thr 95	3264
TAC Tyr	ACT Thr	TCT Ser	CGT Arg	Asn	CGA Arg	GGF Gly	TA?	GAC Asg 150	GT?	A GCC / Ala	с тал а тул	r GAZ c Glu	A AGO 1 Sei 151	ASI	TCT Ser	3312
TCT Ser	GTA Val	CCA Pro 151	Ala	GAT Asp	TAT TYI	GCA Ala	A TC	r Ala	TA:	r GAZ	A GAZ u Glu	A AA 1 Lys 152	S Ala	A TA	r ACA r Thr	3360

GAT Asp	GGA Gly 1530	Arg	AGA Arg	GAC Asp	AAT Asn	CCT Pro 1535	Cys	GAA Glu	TCT Ser	AAC Asn	AGA Arg 1540	GLY	TAT Tyr	GGG Gly	GAT Asp	3408
TAC Tyr 154	Thr	CCA Pro	CTA Leu	CCA Pro	GCT Ala 1550	Gly	TAT Tyr	GTG Val	ACA Thr	AAA Lys 1555	Glu	TTA Leu	GAG Glu	TAC Tyr	TTC Phe 1560	3456
CCA Pro	GAA Glu	ACC Thr	GAT Asp	AAG Lys 156	Val	TGG Trp	ATT Ile	GAG Glu	ATC Ile 1570	Gly	GAA Glu	ACG Thr	GAA Glu	GGA Gly 157	Thr	3504
TTC Phe	ATC Ile	GTG Val	GAC Asp 158	Ser	GTG Val	GAA Glu	TTA Leu	CTT Leu 158	Leu	ATG Met	GAG Glu	GAA Glu	TAA			3546

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1181 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 165 170 175 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 185

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 305 310 315

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val 625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser 645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys 660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn 675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr 690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val 705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln 725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg 740  $\phantom{000}$  745  $\phantom{000}$  750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr 755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp 770 775 780

Pro Leu Ser Ala Pro Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg 785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile

820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 850 855

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 900 905 910

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 995 1000 1005

Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 1010 1015 1020

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 1140 1145 1150

Pro Glu Thr 1155	Asp Lys Val Trp Ile Glu 1160	Ile Gly Glu T	hr Glu Gly Thr 165	
Phe Ile Val 1170	Asp Ser Val Glu Leu Leu 1175	Leu Met Glu G 1180	lu	
(2) INFORMAT	ION FOR SEQ ID NO:29:			
( <i>P</i> (E (C	UENCE CHARACTERISTICS:  LENGTH: 88 base pairs  TYPE: nucleic acid  STRANDEDNESS: single  TOPOLOGY: linear			
(ii) MOI ( <i>I</i>	ECULE TYPE: other nucle A) DESCRIPTION: /desc =	eic acid "primer KE74A2	28"	
(iii) HYI	POTHETICAL: NO			
(xi) SE	QUENCE DESCRIPTION: SEQ	ID NO:29:		
GCAGATCTGG	ATCCATGCAC GCCGTGAAGG GC	CCTTCTAG AAGG	CCTATC GATAAAGAGC	60
TCCCCGGGGA '	TGGATTGCAC GCAGGTTC			88
(2) INFORMA	TION FOR SEQ ID NO:30:			
( (	QUENCE CHARACTERISTICS: A) LENGTH: 40 base pair B) TYPE: nucleic acid C) STRANDEDNESS: single D) TOPOLOGY: linear	S		
(ii) MO (	LECULE TYPE: other nucl A) DESCRIPTION: /desc =	eic acid "primer KE72A	.28"	
(iii) HY	POTHETICAL: NO			
(xi) SE	QUENCE DESCRIPTION: SEQ	ID NO:30:		
GCGTTAACAT	GTCGACTCAG AAGAACTCGT C	AAGAAGGCG		40
(2) INFORM	ATION FOR SEQ ID NO:31:			
	EQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pair (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	rs .		
(ii) Mo	OLECULE TYPE: other nucl (A) DESCRIPTION: /desc =	leic acid = "primer P1(a)	) "	
(iii) H	YPOTHETICAL: NO			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
GTCGACAAGG ATCCAACAAT GG	22
(2) INFORMATION FOR SEQ ID NO:32:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 26 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer P1(b)"</pre>	
(iii) HYPOTHETICAL: NO	
TD NO.22.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	26
AATTGTCGAC AAGGATCCAA CAATGG	20
(2) INFORMATION FOR SEQ ID NO:33:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer P2(a)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
ACACGCTGAC GTCGCGCAGC ACG	23
(2) INFORMATION FOR SEQ ID NO:34:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer P2(b)"</pre>	
(iii) HYPOTHETICAL: NO	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
AGCTACACGC TGACGTCGCG CAG	23
(2) INFORMATION FOR SEQ ID NO:35:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 10 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer A1"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
AATTGTCGAC	10
(2) INFORMATION FOR SEQ ID NO:36:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 10 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid    (A) DESCRIPTION: /desc = "primer A2"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
GCGTGTAGCT	10
(2) INFORMATION FOR SEQ ID NO:37:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid       (A) DESCRIPTION: /desc = "primer P3(a)"</pre>	
(iii) HYPOTHETICAL: NO	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
GCTGCGCGAC GTCAGCGTGT TCGG	24
(2) INFORMATION FOR SEQ ID NO:38:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 23 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer P3(b)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
AATTGCTGCG CGACGTCAGC GTG	23
(2) INFORMATION FOR SEQ ID NO:39:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 25 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "primer P4(a)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
GGCGTTGCCC ATGGTGCCGT ACAGG	25
(2) INFORMATION FOR SEQ ID NO:40:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer P4(b)"</pre>	
(iii) HYDOTHETTCAL: NO	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
AGCTGGCGTT GCCCATGGTG CCG	23
(2) INFORMATION FOR SEQ ID NO:41:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 10 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer B1"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
AATTGCTGCG	10
(2) INFORMATION FOR SEQ ID NO:42:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 10 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer B2"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
AACGCCAGCT	10
(2) INFORMATION FOR SEQ ID NO:43:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 32 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "primer P5(a)"</pre>	
(iii) HYPOTHETICAL: NO	

(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:43:	
TTCCCCCTGT	ACGGCACCAT GGGCAACGCC GC	32
(2) INFORM	ATION FOR SEQ ID NO:44:	
(i) S	EQUENCE CHARACTERISTICS:  (A) LENGTH: 23 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) M	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P5(b)"	
(iii) F	HYPOTHETICAL: NO	
(xi) \$	SEQUENCE DESCRIPTION: SEQ ID NO:44:	
AATTGTACG(	G CACCATGGGC AAC	23
(2) INFOR	MATION FOR SEQ ID NO:45:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 26 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P6(a)"	
(iii)	HYPOTHETICAL: NO	
	SEQUENCE DESCRIPTION: SEQ ID NO:45:	26
(2) INFO	RMATION FOR SEQ ID NO:46:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 23 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer P6(b)"	
(iii)	HYPOTHETICAL: NO	
	PROGRAMMION, SEO ID NO.46.	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:46:	

AGCTGAAGCC GGGGCCCTTC ACC	23
(2) INFORMATION FOR SEQ ID NO:47:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 10 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer C1"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	10
AATTGTACGG	10
(2) INFORMATION FOR SEQ ID NO:48:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 13 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer C2 - first half"</pre>	
(iii) HYPOTHETICAL: NO	
070 TD NO.48:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	13
TTCCCCTGTA CGG	
(2) INFORMATION FOR SEQ ID NO:49:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 10 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "primer C1 - second half"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	

GGCTTCAGCT	10
(2) INFORMATION FOR SEQ ID NO:50:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 19 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid    (A) DESCRIPTION: /desc = "primer PEPCivs#9 - forward"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
GTACAAAAAC CAGCAACTC	19
(2) INFORMATION FOR SEQ ID NO:51:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 19 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer PEPCivs#9 reverse"</pre>	•
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	10
CTGCACAAAG TGGAGTAGT	19
(2) INFORMATION FOR SEQ ID NO:52:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 25 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer P7(a)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	

TGGTGAAGGG CCCCGGCTTC ACCGG

(2) INFORMATION FOR SEQ ID NO:53:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 36 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer P8(a)"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	26
ATCATCGATG AGCTCCTACA CCTGATCGAT GTGGTA	36
(2) INFORMATION FOR SEQ ID NO:54:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer for fourth quarter - second half"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
ATCAGGAGCT CATCGATGAT	20
(2) INFORMATION FOR SEQ ID NO:55:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 11 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	· .
<pre>(ii) MOLECULE TYPE: other nucleic acid</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	

CACCTGATGG ACATCCTGAA

TTCCCCCTGT A	11
(2) INFORMATION FOR SEQ ID NO:56:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "primer MK23A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
GGGGCTGCGG ATGCTGCCCT	20
(2) INFORMATION FOR SEQ ID NO:57:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid       (A) DESCRIPTION: /desc = "primer MK25A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	2.0
GAGCTGACCC TGACCGTGCT	20
(2) INFORMATION FOR SEQ ID NO:58:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "primer MK26A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	

(2) INFORMATION FOR SEQ ID NO:59:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 33 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
TATAAGGATC CCGGGGGCAA GATCTGAGAT ATG	33
(2) INFORMATION FOR SEQ ID NO:60:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 44 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "primer KE134A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	44
CGTGACCGAC TACCACATCG ATCAAGTATC CAATTTAGTT GAGT	44
(2) INFORMATION FOR SEQ ID NO:61:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 44 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer KE135A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
TO THE TAX	44

ACTCAACTAA ATTGGATACT TGATCGATGT GGTAGTCGGT CACG

vo co	
(2) INFORMATION FOR SEQ ID NO:62:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 37 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer KE136A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
	37
GCAGATCTGA GCTCTTAGGT ACCCAATAGC GTAACGT	
(2) INFORMATION FOR SEQ ID NO:63:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer KE137A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
	21
GCTGATTATG CATCAGCCTA T	
(2) INFORMATION FOR SEQ ID NO:64:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 38 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid</pre>	
(iii) HYPOTHETICAL: NO	

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCAGATCTGA GCTCTTATTC CTCCATAAGA AGTAATTC

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer MK05A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
CAAAGGTACC CAATAGCGTA ACG	23
(2) INFORMATION FOR SEQ ID NO:66:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer MK35A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
AACGAGGTGT ACATCGACCG	20
	•
(2) INFORMATION FOR SEQ ID NO:67:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 42 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: other nucleic acid	
(A) DESCRIPTION: /desc = "lolward primer 101	
pCIB4434"  (iii) HYPOTHETICAL: NO	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67: GCACCGATAT CACCATCCAA GGAGGCGATG ACGTATTCAA AG

(2) INFORMATION FOR SEQ ID NO:68:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 51 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid           (A) DESCRIPTION: /desc = "reverse primer for pCIB4434"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	<b></b>
AGCGCATCGA TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGAAA G	51
(2) INFORMATION FOR SEQ ID NO:69:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 30 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid   (A) DESCRIPTION: /desc = "primer #1"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	30
ATTACGTTAC GCTATTGGGT ACCTTTGATG	30
(2) INFORMATION FOR SEQ ID NO:70:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 98 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer #2"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	

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TCCCCGTCCC TGCAGCTGCA GTCTAGGTCC GGGTTCCACT CCAGGTGCGG AGCGCATCGA

TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGA	98
(2) INFORMATION FOR SEQ ID NO:71:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 98 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer #3"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
CAAGTGCGGG GAGCCGAATC GATGCGCTCC GCACCTGGAG TGGAACCCGG ACCTAGACTG	60
CAGCTGCAGG GACGGGGAAA AATGTGCCCCA TCATTCCC	98
(2) INFORMATION FOR SEQ ID NO:72:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 30 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer #4"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	30
TGGTTTCTCT TCGAGAAATT CTAGATTTCC	50
(2) INFORMATION FOR SEQ ID NO:73:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "primer used to map transcriptional start site for TrpA gene"</pre>	
(iii) HYPOTHETICAL: NO	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

# CCGTTCGTTC CTCCTTCGTC GAGG

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- (2) INFORMATION FOR SEQ ID NO:74:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 26 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
    - (v) FRAGMENT TYPE: N-terminal
    - (ix) FEATURE:
      - (A) NAME/KEY: Peptide
      - (B) LOCATION: 1..26
  - (D) OTHER INFORMATION: /note= "N-terminal peptide from pollen specific protein"
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr Thr Pro Leu Thr Phe Gln Val Gly Lys Gly Ser Lys Pro Gly His

Leu Ile Leu Thr Pro Asn Val Ala Thr Ile

- (2) INFORMATION FOR SEQ ID NO:75:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
    - (v) FRAGMENT TYPE: internal
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1..20
  - (D) OTHER INFORMATION: /note= "internal peptide of pollen specific protein"
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Pro Gly His Leu Ile Leu Thr Pro Asn Val Ala Thr Ile Ser Asp

## Val Val Ile Lys 20

- (2) INFORMATION FOR SEQ ID NO:76:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 16 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
    - (v) FRAGMENT TYPE: internal
    - (ix) FEATURE:
      - (A) NAME/KEY: Peptide
      - (B) LOCATION: 1..16
  - (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Gly Gly Thr Arg Ile Ala Asp Asp Val Ile Pro Ala Asp Phe Lys

- (2) INFORMATION FOR SEQ ID NO:77:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
    - (v) FRAGMENT TYPE: internal
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1..12
  - (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Glu His Gly Gly Asp Asp Phe Ser Phe Thr Leu Lys

- (2) INFORMATION FOR SEQ ID NO:78:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (iii) HYPOTHETICAL: NO (v) FRAGMENT TYPE: internal (ix) FEATURE: (A) NAME/KEY: Peptide (B) LOCATION: 1..12 (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78: Glu Gly Pro Thr Gly Thr Trp Thr Leu Asp Thr Lys (2) INFORMATION FOR SEQ ID NO:79: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide #51" (iii) HYPOTHETICAL: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79: 20 (2) INFORMATION FOR SEQ ID NO:80: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

AARTCRTCAB CACCRTGYTC

- - - (ii) MOLECULE TYPE: other nucleic acid
      - (A) DESCRIPTION: /desc = "oligonucleotide #58"
    - (iii) HYPOTHETICAL: NO
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCYTTNCCCA CYTGRAA	17
(2) INFORMATION FOR SEQ ID NO:81:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 33 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "oligonucleotide PE51"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
TGGCCCATGG CTGCGGCGGG GAACGAGTGC GGC	33
(2) INFORMATION FOR SEQ ID NO:82:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 40 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer #42"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	40
AGCGGTCGAC CTGCAGGCAT GCGATCTGCA CCTCCCGCCG	40
(2) INFORMATION FOR SEQ ID NO:83:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 18 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	·
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer #43"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	

ATGGGCAAGG AGCTCGGG	18
(2) INFORMATION FOR SEQ ID NO:84:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 21 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer #SK50"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
CCCTTCAAAA TCTAGAAACC T	21
(2) INFORMATION FOR SEQ ID NO:85:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 27 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid   (A) DESCRIPTION: /desc = "primer #SK49"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
TAATGTCGAC GAACGGCGAG AGATGGA	27
(2) INFORMATION FOR SEQ ID NO:86:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 22 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer KE99A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	

TGCGGTTACC GCCGATCACA TG

(2) INFORMATION FOR SEQ ID NO:87:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 41 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid     (A) DESCRIPTION: /desc = "primer KE97A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
	41
GCGGTACCGC GTCGACGCGG ATCCCGCGGC GGGAAGCTAA G	3.4
(2) INFORMATION FOR SEQ ID NO:88:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 16 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid       (A) DESCRIPTION: /desc = "primer KE100A28"</pre>	
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
GTCGTCGACC GCAACA	16
(2) INFORMATION FOR SEQ ID NO:89:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 39 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic acid</pre>	
(iii) HYPOTHETICAL: NO	

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GCGGTACCGC GTTAACGCGG ATCCTGTCCG ACACCGGAC



(2) INFORMATION FOR SEQ ID NO:90:	•
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic ac</pre>	id mer KE104A28"
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO	O:90:
(X1) SEQUENCE DESCRIPTION. DEV 15 1.	20
GATGTCGTCG ACCGCAACAC	20
(2) INFORMATION FOR SEQ ID NO:91:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
<pre>(ii) MOLECULE TYPE: other nucleic a</pre>	cid .mer KE103A28"
(iii) HYPOTHETICAL: NO	
(xi) SEQUENCE DESCRIPTION: SEQ ID 1	
GCGGTACCGC GGATCCTGTC CGACACCGGA CGGCT	35
(2) INFORMATION FOR SEQ ID NO:92:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 26 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>	
<pre>(ii) MOLECULE TYPE: other nucleic     (A) DESCRIPTION: /desc = "pr</pre>	acid imer KE127"
(iii) HYPOTHETICAL: NO	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCGGATCCGG CTGCGGCGGG GAACGA

(2) INFORMATION FOR SEQ ID NO:93:





(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 23 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "primer	KE150A28"
(iii)	HYPOTHETICAL: NO	

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
- ATTCGCATGC ATGTTTCATT ATC

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- (2) INFORMATION FOR SEQ ID NO:94:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: other nucleic acid
     (A) DESCRIPTION: /desc = "primer KE151A28"
  - (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94: GCTGGTACCA CGGATCCGTC GCTTCTGTGC AACAACC